

Schnizer, Richard

From: Schnizer, Richard
Sent: Tuesday, December 14, 2004 8:50 AM
To: STIC-Biotech/ChemLib
Subject: 09/245,198

Please search for the following:

Polypeptides comprising amino acids 36-284 of SEQ ID NO:4, and nucleic acids that could encode those polypeptides.
Please also perform oligo searches on both.

Nucleic acids comprising nucleotides 106-852 of SEQ ID NO:3. Please also perform an oligo search on nucleotides 106-852 of SEQ ID NO:3.

Please perform full length and oligo searches on SEQ ID NOS:1 and 2. Please also search for nucleic acids that could encode SEQ ID NO:2, and perform an oligo search as well.

Please provide the results on disk.

Thank you-

Richard Schnizer, Ph.D.
Patent Examiner
Art Unit 1635
Remsen 2D30
571-272-0762
Mail Box 2C18

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 11:20:48 ; Search time 651 Seconds
(without alignments)
9418.316 Million cell updates/sec

Title: US-09-245-198A-1

Perfect score: 1168

Sequence: 1 ggtgctgagcctggcctgg.....ataaatcatgattcttc 1168

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1168	100.0	1168	2	AAV18599	Aav18599 Mus muscu
2	1168	100.0	1239	10	ADC97713	Adc97713 Murine FL
3	650	55.7	701	2	AAX23425	Aax23425 Mouse TNR
c 4	87	7.4	412	10	ADB56326	Adb56326 Toxicity-
5	65	5.6	65	6	ABN55975	Abn55975 Mouse spl
6	46	3.9	898	4	AAS03964	Aas03964 Expressio

7	46	3.9	1030	2	AAX23424	Aax23424 Human TNR	
8	46	3.9	1236	2	AAV47613	Aav47613 TNF relat	
9	46	3.9	1236	4	AAD04350	Aad04350 Human TRE	
10	46	3.9	1306	8	ACC57901	Acc57901 Human TWE	
11	46	3.9	1306	10	ADC35205	Adc35205 Human cDN	
12	46	3.9	1306	10	AAD63914	Aad63914 Human TWE	
13	46	3.9	1306	10	ACC57587	Acc57587 Polynucle	
14	46	3.9	1353	3	AAA49717	Aaa49717 Human PRO	
15	46	3.9	1353	6	ABK40255	Abk40255 cDNA enco	
16	46	3.9	1353	10	ADJ37284	Adj37284 Human tum	
17	46	3.9	1353	12	ADG68208	Adg68208 Human PRO	
18	46	3.9	1364	6	ABK34881	Abk34881 Human cDN	
19	46	3.9	1373	2	AAV18600	Aav18600 Homo sapi	
20	46	3.9	1421	2	AAX56000	Aax56000 Human tum	
c 21	24	2.1	24	2	AAX23453	Aax23453 Mouse TNR	
c 22	24	2.1	24	2	AAX23452	Aax23452 Mouse TNR	
c 23	21	1.8	21	2	AAV18608	Aav18608 Synthetic	
c 24	21	1.8	654	11	ABD16419	Abd16419 Pseudomon	
	25	21	1.8	1236	11	ABD16126	Abd16126 Pseudomon
	26	21	1.8	1278	11	ABD16008	Abd16008 Pseudomon
	27	20	1.7	20	2	AAV18606	Aav18606 Synthetic
	28	20	1.7	20	2	AAV18605	Aav18605 Synthetic
	29	20	1.7	981	11	ABD09286	Abd09286 Pseudomon
	30	20	1.7	1560	11	ACH94819	Ach94819 Klebsiell
	31	20	1.7	1781	10	ADE58028	Ade58028 Human gen
	32	20	1.7	1781	10	ADE58032	Ade58032 Human gen
c 33	20	1.7	2739	11	ABD08988	Abd08988 Pseudomon	
	34	20	1.7	2778	11	ABD09354	Abd09354 Pseudomon
	35	20	1.7	6365	6	ABL32124	Abl32124 Human imm
	36	19	1.6	282	2	AAT22190	Aat22190 Human gen
c 37	19	1.6	310	6	ABN75488	Abn75488 Human ORF	
	38	19	1.6	408	8	ABX37032	Abx37032 Bovine ES
c 39	19	1.6	474	9	ACH36181	Ach36181 Human end	
c 40	19	1.6	563	4	AAK92176	Aak92176 Human cDN	
c 41	19	1.6	563	4	AAK93441	Aak93441 Human cDN	
c 42	19	1.6	563	12	ADL29868	Adl29868 5' end of	
c 43	19	1.6	563	12	ADL28603	Adl28603 5' end of	
c 44	19	1.6	789	4	AAK92269	Aak92269 Human cDN	
c 45	19	1.6	789	4	AAK93534	Aak93534 Human cDN	

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:10:58 ; Search time 4238 Seconds
(without alignments)
10042.852 Million cell updates/sec

Title: US-09-245-198A-1

Perfect score: 1168

Sequence: 1 ggtgctgagcctggcctgg.....ataaatcatgatttctttc 1168

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	579	49.6	748	7	CN270781	CN270781 170005999
2	492	42.1	665	6	BY742288	BY742288 BY742288
3	492	42.1	1033	3	AK020909	AK020909 Mus muscu
4	487	41.7	892	6	CB204861	CB204861 AGENCOURT
5	477	40.8	2237	3	AK044387	AK044387 Mus muscu
6	476	40.8	482	9	CG653257	CG653257 OST418407
7	473	40.5	620	7	CK625052	CK625052 mi28e10.y
8	454	38.9	561	2	AW763237	AW763237 ur70d09.y
9	449	38.4	918	2	BF577781	BF577781 602092080

10	416	35.6	939	6	CB849011	CB849011 MRA-0673
11	360	30.8	360	2	BE654876	BE654876 UI-M-BH0-
12	351	30.1	494	9	CG596702	CG596702 OST259234
13	351	30.1	543	9	CG565104	CG565104 OST189654
14	348	29.8	349	6	BY766420	BY766420 BY766420
15	331	28.3	445	1	AA870722	AA870722 vq25g07.r
16	328	28.1	692	6	BY748962	BY748962 BY748962
17	316	27.1	650	4	BG404836	BG404836 602420160
18	314	26.9	533	2	BE628951	BE628951 uu30c03.y
19	310	26.5	367	4	BI111534	BI111534 602895883
20	310	26.5	967	6	CB848966	CB848966 MRA-0623
c 21	306	26.2	315	2	BF466521	BF466521 UI-M-CG0p
c 22	301	25.8	405	1	AI854476	AI854476 UI-M-BH0-
c 23	299	25.6	456	5	BX634398	BX634398 BX634398
24	297	25.4	531	9	CG590009	CG590009 OST242925
25	294	25.2	471	1	AA221610	AA221610 my18d09.r
26	279	23.9	376	1	AA792068	AA792068 vn69d09.r
27	260	22.3	393	9	CG493044	CG493044 OST31172
28	252	21.6	474	4	BI965174	BI965174 id34e07.y
29	252	21.6	778	6	CB572618	CB572618 AGENCOURT
30	251	21.5	731	9	AG517989	AG517989 Mus muscu
31	245	21.0	424	9	CG512379	CG512379 OST65281
32	242	20.7	581	4	BI738634	BI738634 603358846
c 33	240	20.5	240	2	AW764050	AW764050 ur70d09.x
34	236	20.2	424	9	CG593688	CG593688 OST251087
35	231	19.8	269	9	CG564287	CG564287 OST188290
36	229	19.6	897	4	BI730298	BI730298 603350276
37	221	18.9	554	9	CG629394	CG629394 OST341515
38	200	17.1	626	7	CK621323	CK621323 ml23a04.y
39	183	15.7	752	9	AG592486	AG592486 Mus muscu
40	179	15.3	400	1	AI152313	AI152313 ud87h02.r
41	178	15.2	418	9	CG611020	CG611020 OST295426
42	175	15.0	403	9	CG548201	CG548201 OST149561
43	175	15.0	493	2	BE307031	BE307031 601087888
c 44	171	14.6	487	2	AW320117	AW320117 un17b02.x
45	168	14.4	352	9	CG543056	CG543056 OST138358

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 12:19:28 ; Search time 5273 Seconds
(without alignments)
10474.942 Million cell updates/sec

Title: US-09-245-198A-1

Perfect score: 1168

Sequence: 1 ggtgctgagcctggcctgg.....ataaatcatgatttctcttc 1168

Scoring table: OLIGO_NUC
Gapext 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
ID						
1	1168	100.0	1168	6	BD062757	BD062757 A tumor n
2	1168	100.0	1239	10	AF030100	AF030100 Mus muscu
c 3	384	32.9	203083	2	AC069459	AC069459 Mus muscu
c 4	384	32.9	234182	10	AL603707	AL603707 Mouse DNA

5	122	10.4	750	10	AY607588	AY607588 Rattus no
6	109	9.3	1576	10	BC079107	BC079107 Rattus no
7	109	9.3	130254	2	AC136195	AC136195 Rattus no
c 8	109	9.3	165316	2	AC119115	AC119115 Rattus no
9	109	9.3	223877	2	AC098923	AC098923 Rattus no
c 10	109	9.3	225077	2	AC136563	AC136563 Rattus no
c 11	67	5.7	234801	2	AC118309	AC118309 Rattus no
12	65	5.6	65	6	CQ559088	CQ559088 Sequence
13	46	3.9	898	6	AX180714	AX180714 Sequence
14	46	3.9	1236	6	AR140407	AR140407 Sequence
15	46	3.9	1236	6	BD057124	BD057124 Member of
16	46	3.9	1306	9	AF030099	AF030099 Homo sapi
17	46	3.9	1353	6	AX201324	AX201324 Sequence
18	46	3.9	1353	9	AY358870	AY358870 Homo sapi
19	46	3.9	1368	9	AF055872	AF055872 Homo sapi
20	46	3.9	1373	6	BD062758	BD062758 A tumor n
21	46	3.9	1421	6	BD090952	BD090952 Apo-3 lig
22	46	3.9	1615	9	BC071837	BC071837 Homo sapi
23	46	3.9	1642	9	BC019047	BC019047 Homo sapi
24	39	3.3	180222	2	AC130192	AC130192 Sus scrof
25	35	3.0	149736	2	AC126239	AC126239 Felis cat
c 26	33	2.8	60268	9	AC016876	AC016876 Homo sapi
27	33	2.8	148555	2	AC126921	AC126921 Bos tauru
28	33	2.8	176258	2	AC126925	AC126925 Canis fam
29	33	2.8	218485	2	AC127470	AC127470 Pan trogl
30	29	2.5	213	6	CQ710250	CQ710250 Sequence
31	29	2.5	1816	9	AY081051	AY081051 Homo sapi
32	25	2.1	164272	10	AC115714	AC115714 Mus muscu
33	25	2.1	212093	2	AC126237	AC126237 Canis fam
34	24	2.1	751	11	BV166827	BV166827 TNFSF12_2
c 35	24	2.1	163542	2	AC129071	AC129071 Pan trogl
c 36	24	2.1	259875	2	AC115406	AC115406 Rattus no
37	23	2.0	201	11	BV202888	BV202888 sqnm21025
38	23	2.0	137573	10	AL669884	AL669884 Mouse DNA
39	23	2.0	167959	2	CR383682	CR383682 Mus muscu
40	23	2.0	190991	10	AL773505	AL773505 Mouse DNA
c 41	23	2.0	202655	10	AC026682	AC026682 Mus muscu
42	23	2.0	218798	2	AC121007	AC121007 Rattus no
c 43	23	2.0	235953	2	AC126654	AC126654 Rattus no
44	23	2.0	257097	2	AC096199	AC096199 Rattus no
c 45	23	2.0	261157	2	AC103330	AC103330 Rattus no

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
	1	1168	100.0	1168	6	BD062757 A tumor n
	2	1168	100.0	1239	10	AF030100 Mus muscu
	3	973	83.3	1576	10	BC079107 Rattus no
c	4	711	60.9	203083	2	AC069459 Mus muscu
c	5	711	60.9	234182	10	AL603707 Mouse DNA
	6	647	55.4	750	10	AY607588 Rattus no
	7	628.6	53.8	1353	6	AX201324 Sequence
	8	628.6	53.8	1353	9	AY358870 Homo sapi
	9	628.6	53.8	1368	9	AF055872 Homo sapi
	10	628.6	53.8	1421	6	BD090952 Apo-3. lig
	11	624	53.4	1306	9	AF030099 Homo sapi
	12	614.6	52.6	1373	6	BD062758 A tumor n
	13	597.8	51.2	1236	6	AR140407 Sequence
	14	597.8	51.2	1236	6	BD057124 Member of
	15	566.6	48.5	130254	2	AC136195 Rattus no
c	16	566.6	48.5	165316	2	AC119115 Rattus no
	17	566.6	48.5	223877	2	AC098923 Rattus no
c	18	566.6	48.5	225077	2	AC136563 Rattus no
	19	498.8	42.7	898	6	AX180714 Sequence
c	20	428	36.6	234801	2	AC118309 Rattus no
	21	409.4	35.1	1642	9	BC019047 Homo sapi
	22	405	34.7	1615	9	BC071837 Homo sapi
	23	328.4	28.1	1816	9	AY081051 Homo sapi
	24	304	26.0	218485	2	AC127470 Pan trogl
c	25	303.8	26.0	60268	9	AC016876 Homo sapi
	26	278.2	23.8	148555	2	AC126921 Bos tauru
	27	261	22.3	149736	2	AC126239 Felis cat
	28	249.4	21.4	751	11	BV166827 TNFSF12_2
	29	237.4	20.3	180222	2	AC130192 Sus scrof
	30	212	18.2	176258	2	AC126925 Canis fam
	31	111.6	9.6	212093	2	AC126237 Canis fam
	32	101.2	8.7	213	6	CQ710250 Sequence
	33	90	7.7	201	11	BV202888 sqnm21025
	34	88.4	7.6	7218	6	I66494 Sequence 14
	35	69.8	6.0	195	6	AX379024 Sequence
	36	65	5.6	65	6	CQ559088 Sequence
	37	56.2	4.8	125020	9	AF429315 Homo sapi
c	38	55.8	4.8	228056	2	AC144061 Macaca mu
c	39	55.8	4.8	303091	2	AC084799 Mus muscu
	40	55.2	4.7	115145	10	AL807240 Mouse DNA
c	41	55	4.7	185822	2	AC073554 Homo sapi
	42	54.8	4.7	100511	2	AC010774 Homo sapi
	43	54.4	4.7	87120	2	AC012225 Homo sapi
	44	54.2	4.6	191415	10	AC096625 Mus muscu
c	45	54.2	4.6	298166	2	AC087563 Homo sapi

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	
	1	1168	100.0	1168	2	AAV18599	Aav18599 Mus muscu
	2	1168	100.0	1239	10	ADC97713	Adc97713 Murine FL
	3	699.4	59.9	701	2	AAX23425	Aax23425 Mouse TNR
	4	628.6	53.8	1353	3	AAA49717	Aaa49717 Human PRO
	5	628.6	53.8	1353	6	ABK40255	Abk40255 cDNA enco
	6	628.6	53.8	1353	10	ADJ37284	Adj37284 Human tum
	7	628.6	53.8	1353	12	ADG68208	Adg68208 Human PRO
	8	628.6	53.8	1421	2	AAX56000	Aax56000 Human tum
	9	624	53.4	1306	8	ACC57901	Acc57901 Human TWE
	10	624	53.4	1306	10	ADC35205	Adc35205 Human cDN
	11	624	53.4	1306	10	AAD63914	Aad63914 Human TWE
	12	624	53.4	1306	10	ACC57587	Acc57587 Polynucle
	13	618.2	52.9	1364	6	ABK34881	Abk34881 Human cDN
	14	614.6	52.6	1373	2	AAV18600	Aav18600 Homo sapi
	15	597.8	51.2	1236	2	AAV47613	Aav47613 TNF relat
	16	597.8	51.2	1236	4	AAD04350	Aad04350 Human TRE
	17	522.8	44.8	1030	2	AAX23424	Aax23424 Human TNR
	18	498.8	42.7	898	4	AAS03964	Aas03964 Expressio
c	19	274.4	23.5	412	10	ADB56326	Adb56326 Toxicity-
	20	188.8	16.2	408	8	ABX37032	Abx37032 Bovine ES
	21	82.8	7.1	282	2	AAT22190	Aat22190 Human gen
	22	69.8	6.0	195	6	ABK29540	Abk29540 Colon ade
	23	65.6	5.6	493	9	ACH34013	Ach34013 Human end
	24	65	5.6	65	6	ABN55975	Abn55975 Mouse spl
	25	60.4	5.2	1064	6	ABT09678	Abt09678 Human PAL
	26	57.4	4.9	264	8	ABX52254	Abx52254 Bovine ES
c	27	52.6	4.5	2000	8	ADA71938	Ada71938 Rice gene
c	28	46.8	4.0	1117	10	ADC86688	Adc86688 Human GPC
c	29	46.6	4.0	3133	10	ADC86738	Adc86738 Human GPC
	30	46.6	4.0	53522	6	AAD30228	Aad30228 Human PKD
	31	46.6	4.0	53526	2	AAT94101	Aat94101 Human PKD
	32	46.6	4.0	53577	2	AAT18551	Aat18551 Human pol
	33	46.6	4.0	53577	2	AAT94108	Aat94108 Human PKD
	34	45.8	3.9	1065	6	ABT09682	Abt09682 Human PAL
	35	45.8	3.9	105325	6	ABK94407	Abk94407 DNA encod
	36	45.8	3.9	105325	12	ADQ18755	Adq18755 Human sof
c	37	45.6	3.9	5452	10	ADC86736	Adc86736 Human GPC
	38	45	3.9	1337	2	AAZ17263	Aaz17263 Human gen
c	39	44.8	3.8	1000	3	AAA02484	Aaa02484 Human col
c	40	44.8	3.8	3163	10	ADC87060	Adc87060 Human GPC
c	41	44.8	3.8	12733	6	ABK98631	Abk98631 Vector pE
c	42	44.8	3.8	12733	9	ACD13882	Acd13882 L. lactis
c	43	44.8	3.8	12739	6	ABK98592	Abk98592 Vector pE
c	44	44.8	3.8	12739	9	ACD13843	Acd13843 Plasmid p
	45	43.8	3.8	28198	10	ADG37080	Adg37080 Mouse pla

Search completed: December 21, 2004, 11:12:43
Job time : 718.828 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:35:48 ; Search time 4423.76 Seconds
(without alignments)
9621.134 Million cell updates/sec

Title: US-09-245-198A-1

Perfect score: 1168

Sequence: 1 ggtgctgagcctggcctgg.....ataaatcatgatttctttc 1168

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	883.8	75.7	1033	3	AK020909	AK020909 Mus muscu
2	724.4	62.0	892	6	CB204861	CB204861 AGENCOURT
3	695	59.5	748	7	CN270781	CN270781 170005999
4	647.4	55.4	790	7	CO559990	CO559990 AGENCOURT
5	625.8	53.6	918	2	BF577781	BF577781 602092080
6	605.6	51.8	665	6	BY742288	BY742288 BY742288

7	602.4	51.6	760	7	CO572381	CO572381 AGENCOURT	
8	549	47.0	2237	3	AK044387	AK044387 Mus muscu	
9	545	46.7	620	7	CK625052	CK625052 mi28e10.y	
10	533.4	45.7	543	9	CG565104	CG565104 OST189654	
11	529.4	45.3	805	7	CO393621	CO393621 AGENCOURT	
12	519.4	44.5	731	4	BI871711	BI871711 603395825	
13	510	43.7	554	9	CG629394	CG629394 OST341515	
14	507.4	43.4	728	4	BI870393	BI870393 603395641	
15	504	43.2	561	2	AW763237	AW763237 ur70d09.y	
16	497	42.6	533	2	BE628951	BE628951 uu30c03.y	
17	489.6	41.9	650	4	BG404836	BG404836 602420160	
c	18	488.8	41.8	687	5	BQ208433	BQ208433 UI-R-EP0-
	19	481.2	41.2	584	2	AW917574	AW917574 EST348878
	20	480.8	41.2	939	6	CB849011	CB849011 MRA-0673
	21	480.4	41.1	777	4	BI819200	BI819200 603034614
	22	476	40.8	482	9	CG653257	CG653257 OST418407
	23	475	40.7	774	7	CO574209	CO574209 AGENCOURT
	24	473	40.5	834	4	BI766766	BI766766 603056866
c	25	471.6	40.4	683	7	CK843985	CK843985 UI-R-BJ1-
	26	467.8	40.1	948	5	BQ707185	BQ707185 AGENCOURT
	27	464.8	39.8	666	6	CF126539	CF126539 UI-HF-ET0
	28	460.4	39.4	731	9	AG517989	AG517989 Mus muscu
	29	456.4	39.1	828	4	BI596681	BI596681 603243254
	30	448.2	38.4	621	9	CG584545	CG584545 OST230701
	31	440.6	37.7	545	6	CB141389	CB141389 K-EST0194
	32	437.8	37.5	471	1	AA221610	AA221610 my18d09.r
	33	430.2	36.8	498	9	CG554711	CG554711 OST168603
c	34	426.8	36.5	624	5	BU759448	BU759448 UI-R-FF0-
	35	422.6	36.2	697	6	CF126932	CF126932 UI-HF-ET0
	36	421.6	36.1	474	9	CG609156	CG609156 OST290052
	37	421.6	36.1	963	5	BQ671259	BQ671259 AGENCOURT
	38	420	36.0	483	9	CG646715	CG646715 OST393421
	39	419.2	35.9	940	5	BQ884231	BQ884231 AGENCOURT
c	40	410.4	35.1	456	5	BX634398	BX634398 BX634398
	41	406.8	34.8	471	9	CG568080	CG568080 OST194813
	42	406.4	34.8	1071	4	BM921213	BM921213 AGENCOURT
	43	400.4	34.3	418	9	CG611020	CG611020 OST295426
	44	393.2	33.7	494	9	CG596702	CG596702 OST259234
	45	390.6	33.4	445	1	AA870722	AA870722 vq25g07.r

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OM protein - protein search, using sw model

Run on: December 21, 2004, 16:26:57 ; Search time 52.2152 Seconds
(without alignments)
1545.797 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 225

Sequence: 1 VLSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	225	100.0	225	2	AAW47524	Aaw47524 Mus muscu
2	225	100.0	225	3	AAB07527	Aab07527 Amino aci
3	225	100.0	249	7	ADC97712	Adc97712 Murine FL
4	178	79.1	211	2	AAW93591	Aaw93591 Mouse TNR
5	32	14.2	146	4	AAE00895	Aae00895 Human TRE
6	32	14.2	189	2	AAW29746	Aaw29746 TNF relat
7	32	14.2	189	4	AAE00892	Aae00892 Human UL4
8	32	14.2	208	2	AAW93590	Aaw93590 Human TNR
9	32	14.2	249	2	AAW29745	Aaw29745 TNF relat
10	32	14.2	249	2	AAY09369	Aay09369 Human tum

11	32	14.2	249	3	AAY95338	Aay95338 Human PRO
12	32	14.2	249	3	AAB07526	Aab07526 Amino aci
13	32	14.2	249	4	AAE00891	Aae00891 Human TRE
14	32	14.2	249	5	AAU86129	Aau86129 Human PRO
15	32	14.2	249	6	ABR42315	Abr42315 Human TWE
16	32	14.2	249	7	ADC35206	Adc35206 Human TNF
17	32	14.2	249	7	ABW02278	Abw02278 Human TWE
18	32	14.2	249	7	ADJ37285	Adj37285 Human tum
19	32	14.2	249	8	ADG68209	Adg68209 Human PRO
20	32	14.2	273	4	AAU03499	Aau03499 TWEAK ext
21	32	14.2	284	2	AAW47525	Aaw47525 Homo sapi
22	8	3.6	24	2	AAY34189	Aay34189 Human pre
23	8	3.6	84	4	AAU61282	Aau61282 Propionib
24	8	3.6	84	6	ABM57801	Abm57801 Propionib
25	8	3.6	85	6	ABP58626	Abp58626 Human end
26	8	3.6	85	6	ABR58356	Abr58356 Bcu631 pr
27	8	3.6	110	7	ADF07632	Adf07632 Bacterial
28	8	3.6	129	4	AAM95789	Aam95789 Human rep
29	8	3.6	129	4	ABB96320	Abb96320 Human tes
30	8	3.6	190	5	ABP28041	Abp28041 Streptoco
31	8	3.6	251	8	ADN99276	Adn99276 Novel hum
32	8	3.6	365	5	AAE28094	Aae28094 Murine ne
33	8	3.6	366	7	ADE63466	Ade63466 Rat Prote
34	8	3.6	366	7	ADE63475	Ade63475 Rat Prote
35	8	3.6	366	7	ADE63469	Ade63469 Rat Prote
36	8	3.6	366	7	ADE63472	Ade63472 Rat Prote
37	8	3.6	370	4	ABG13391	Abg13391 Novel hum
38	8	3.6	370	4	ABG05012	Abg05012 Novel hum
39	8	3.6	370	4	ABG18115	Abg18115 Novel hum
40	8	3.6	376	7	ABO79285	Abo79285 Pseudomon
41	8	3.6	431	7	ADC64562	Adc64562 Synechoco
42	8	3.6	431	8	ADQ07363	Adq07363 Synechoco
43	8	3.6	473	4	ABB58662	Abb58662 Drosophil
44	8	3.6	523	8	ADO61963	Ado61963 Transcrip
45	8	3.6	527	5	ABB07815	Abb07815 Chicken s

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OM protein - protein search, using sw model

Run on: December 21, 2004, 16:31:34 ; Search time 15.1899 Seconds
(without alignments)
982.335 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 225

Sequence: 1 VLSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

¶

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	32	14.2	146	3	US-09-105-343A-6	Sequence 6, Appli
2	32	14.2	189	3	US-09-105-343A-3	Sequence 3, Appli
3	32	14.2	249	3	US-09-105-343A-2	Sequence 2, Appli
4	32	14.2	273	4	US-09-883-777-2	Sequence 2, Appli
5	8	3.6	24	3	US-09-252-586-29	Sequence 29, Appli
6	8	3.6	110	4	US-09-543-681A-7917	Sequence 7917, Ap
7	8	3.6	366	1	US-08-004-492-8	Sequence 8, Appli
8	8	3.6	376	4	US-09-252-991A-28031	Sequence 28031, A
9	8	3.6	527	4	US-09-930-218-16	Sequence 16, Appli
10	8	3.6	530	3	US-09-252-586-2	Sequence 2, Appli
11	8	3.6	532	3	US-09-181-336-15	Sequence 15, Appli
12	8	3.6	543	2	US-08-922-170B-10	Sequence 10, Appli

13	8	3.6	543	3	US-09-071-739B-2	Sequence 2, Appli
14	8	3.6	543	3	US-09-181-336-13	Sequence 13, Appli
15	8	3.6	543	3	US-09-260-038B-2	Sequence 2, Appli
16	8	3.6	543	4	US-09-635-923-2	Sequence 2, Appli
17	8	3.6	543	4	US-09-487-716A-2	Sequence 2, Appli
18	8	3.6	543	4	US-09-322-977-2	Sequence 2, Appli
19	8	3.6	543	4	US-09-186-200-1	Sequence 1, Appli
20	8	3.6	543	4	US-09-435-739-10	Sequence 10, Appli
21	8	3.6	543	4	US-09-930-218-3	Sequence 3, Appli
22	8	3.6	543	4	US-09-704-772A-2	Sequence 2, Appli
23	8	3.6	543	4	US-09-988-113-10	Sequence 10, Appli
24	8	3.6	545	4	US-09-899-440-18	Sequence 18, Appli
25	8	3.6	548	4	US-09-252-991A-20793	Sequence 20793, A
26	8	3.6	588	4	US-09-601-777-2	Sequence 2, Appli
27	8	3.6	592	4	US-09-435-739-14	Sequence 14, Appli
28	8	3.6	592	4	US-09-988-113-14	Sequence 14, Appli
29	8	3.6	626	4	US-09-252-991A-20601	Sequence 20601, A
30	7	3.1	15	1	US-08-208-181A-17	Sequence 17, Appli
31	7	3.1	17	3	US-09-342-681C-121	Sequence 121, App
32	7	3.1	20	4	US-09-149-476-726	Sequence 726, App
33	7	3.1	25	1	US-08-208-181A-2	Sequence 2, Appli
34	7	3.1	64	4	US-09-248-796A-14250	Sequence 14250, A
35	7	3.1	65	4	US-09-248-796A-25920	Sequence 25920, A
36	7	3.1	70	4	US-09-248-796A-21119	Sequence 21119, A
37	7	3.1	77	4	US-09-248-796A-22909	Sequence 22909, A
38	7	3.1	105	4	US-09-543-681A-8267	Sequence 8267, Ap
39	7	3.1	115	3	US-09-219-983A-4	Sequence 4, Appli
40	7	3.1	131	1	US-08-012-543-4	Sequence 4, Appli
41	7	3.1	131	1	US-08-371-121-25	Sequence 25, Appli
42	7	3.1	131	5	PCT-US93-07645A-4	Sequence 4, Appli
43	7	3.1	131	5	PCT-US93-07645-4	Sequence 4, Appli
44	7	3.1	136	4	US-09-252-991A-31120	Sequence 31120, A
45	7	3.1	138	4	US-09-252-991A-20949	Sequence 20949, A

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OM protein - protein search, using sw model

Run on: December 21, 2004, 16:29:37 ; Search time 14.2405 Seconds
(without alignments)
1520.225 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 225

Sequence: 1 VLSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	10	4.4	111	2	A85866	hypothetical prote
2	9	4.0	733	2	S78376	photosystem I P700
3	8	3.6	229	2	AE2758	conserved hypothet
4	8	3.6	229	2	B97539	hypothetical prote
5	8	3.6	365	2	I56197	Fc gamma (IgG) rec
6	8	3.6	366	2	A37374	Fc gamma (IgG) rec
7	8	3.6	486	2	T48119	hypothetical prote
8	7	3.1	82	2	AH0573	probable membrane
9	7	3.1	109	2	E70730	hypothetical prote
10	7	3.1	128	1	A57321	E48 antigen precur
11	7	3.1	131	2	E30552	T-cell activation
12	7	3.1	131	2	I52290	interleukin-13 - r
13	7	3.1	137	2	G70090	hypothetical prote
14	7	3.1	141	2	A32854	hemoglobin alpha c

15	7	3.1	147	2	A71217	hypothetical prote
16	7	3.1	157	2	A75567	conserved hypothet
17	7	3.1	162	2	T24937	hypothetical prote
18	7	3.1	165	2	AD0129	cationic 19 kDa ou
19	7	3.1	170	2	S44789	D2007.4 protein -
20	7	3.1	177	2	E71211	hypothetical prote
21	7	3.1	180	1	LGGT	beta-lactoglobulin
22	7	3.1	180	1	LGSH	beta-lactoglobulin
23	7	3.1	194	2	E83758	chromate transport
24	7	3.1	197	2	S28465	quaternary amine t
25	7	3.1	207	2	I46084	interleukin 6 - ca
26	7	3.1	211	2	T29426	hypothetical prote
27	7	3.1	213	2	T31447	plastoquinol-plast
28	7	3.1	234	2	G85098	H+-transporting AT
29	7	3.1	244	2	A46066	lymphotoxin beta -
30	7	3.1	251	1	TRHUAZ	azurocidin precurs
31	7	3.1	262	2	A64718	flagellar basal bo
32	7	3.1	262	2	F71801	flagellar basal-bo
33	7	3.1	281	2	H97625	hypothetical prote
34	7	3.1	304	2	JX0209	lectin, galactose/
35	7	3.1	311	2	C84101	hypothetical prote
36	7	3.1	311	2	H84746	hypothetical prote
37	7	3.1	339	2	D70942	probable pfkB prot
38	7	3.1	347	2	T32768	hypothetical prote
39	7	3.1	348	2	E84299	hypothetical prote
40	7	3.1	352	2	E70797	hypothetical prote
41	7	3.1	357	2	T32881	hypothetical prote
42	7	3.1	371	2	S46436	porin fomA precurs
43	7	3.1	372	2	A95338	hypothetical proté
44	7	3.1	375	2	T35895	ferrochelatase - S
45	7	3.1	376	2	A75360	hypothetical prote

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OM protein - protein search, using sw model

Run on: December 21, 2004, 16:29:02 ; Search time 56.962 Seconds
(without alignments)
2272.730 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 225

Sequence: 1 VLSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	225	100.0	249	1	TN12_MOUSE	054907 mus musculu
2	159	70.7	410	2	Q8BXS2	Q8bxs2 mus musculu
3	122	54.2	249	2	Q6J1A8	Q6j1a8 rattus norv
4	122	54.2	249	2	AAT35582	Aat35582 rattus no
5	32	14.2	249	1	TN12_HUMAN	O43508 homo sapien
6	32	14.2	330	2	Q8IZK7	Q8izk7 homo sapien
7	21	9.3	134	2	Q6IPN8	Q6ipn8 homo sapien
8	21	9.3	134	2	AAH71837	Aah71837 homo sapi
9	11	4.9	438	2	Q7VVB7	Q7vvb7 bordetella
10	11	4.9	470	2	Q7W7F2	Q7w7f2 bordetella
11	10	4.4	111	1	YFBW_ECOLI	Q47377 escherichia
12	10	4.4	111	2	Q7UC61	Q7uc61 shigella fl
13	10	4.4	111	2	Q8FFL8	Q8ffl8 escherichia
14	10	4.4	111	2	Q8X4J8	Q8x4j8 escherichia
15	9	4.0	414	2	Q6TNW7	Q6tnw7 pavlova gyr
16	9	4.0	414	2	AAR30310	Aar30310 pavlova g

17	9	4.0	422	2	Q6TNW5	Q6tnw5 heterosigma
18	9	4.0	422	2	Q6TNW6	Q6tnw6 pavlova lut
19	9	4.0	422	2	Q6TNY6	Q6tny6 cyanidium s
20	9	4.0	422	2	AAR30291	Aar30291 cyanidium
21	9	4.0	422	2	AAR30311	Aar30311 pavlova l
22	9	4.0	422	2	AAR30312	Aar30312 heterosig
23	9	4.0	733	1	PSAB_ODOSI	P49480 odontella s
24	9	4.0	734	1	PSAB_CYACA	Q9tlq6 cyanidium c
25	9	4.0	749	2	Q7V511	Q7v511 prochloroco
26	8	3.6	123	2	Q88X09	Q88x09 lactobacill
27	8	3.6	143	2	Q8FI66	Q8fi66 escherichia
28	8	3.6	149	2	Q9D1T4	Q9d1t4 mus musculu
29	8	3.6	190	2	Q8DZK5	Q8dzk5 streptococc
30	8	3.6	190	2	Q8E569	Q8e569 streptococc
31	8	3.6	229	2	Q7CZ60	Q7cz60 agrobacteri
32	8	3.6	229	2	Q8UFC1	Q8ufc1 agrobacteri
33	8	3.6	281	2	Q711H2	Q711h2 lactobacill
34	8	3.6	281	2	CAF33351	Caf33351 lactobaci
35	8	3.6	324	2	Q7V4A3	Q7v4a3 prochloroco
36	8	3.6	328	2	Q7UX67	Q7ux67 rhodopirell
37	8	3.6	329	2	Q9EX48	Q9ex48 streptomyce
38	8	3.6	365	1	FCGN_MOUSE	Q61559 mus musculu
39	8	3.6	366	1	FCGN_RAT	P13599 rattus norv
40	8	3.6	366	2	AAH61975	Aah61975 rattus no
41	8	3.6	369	2	Q6PKB0	Q6pkb0 mus musculu
42	8	3.6	369	2	AAH03786	Aah03786 mus muscu
43	8	3.6	399	2	Q8PFQ8	Q8pfq8 xanthomonas
44	8	3.6	421	2	Q6TNY5	Q6tny5 galdieria m
45	8	3.6	421	2	AAR30292	Aar30292 galdieria

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 18:47:38 ; Search time 4057.59 Seconds
(without alignments)
2622.288 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 225

Sequence: 1 VLSLGLALACLGLLLVVVSL..... PWAHLKAAPFLTYFGLFQVH 225

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9045936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-

Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162224_10205/app_query.fasta_1.7
82
-DB=GenEmbl -QFMT=fastap -SUFFIX=olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198 @CGN_1_1_4236 @runat_20122004_162224_10205 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPEBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

```

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	ID
	1	225	100.0	1168	6	BD062757
	2	225	100.0	1239	10	AF030100
	3	133	59.1	1576	10	BC079107
	4	122	54.2	750	10	AY607588
	5	84	37.3	130254	2	AC136195
c	6	84	37.3	165316	2	AC119115
c	7	84	37.3	203083	2	AC069459
	8	84	37.3	223877	2	AC098923
c	9	84	37.3	225077	2	AC136563
c	10	84	37.3	234182	10	AL603707
c	11	84	37.3	234801	2	AC118309
	12	46	20.4	180222	2	AC130192
	13	45	20.0	176258	2	AC126925
	14	38	16.9	149736	2	AC126239
	15	32	14.2	751	11	BV166827
	16	32	14.2	898	6	AX180714
	17	32	14.2	1236	6	AR140407
	18	32	14.2	1236	6	BD057124
	19	32	14.2	1306	9	AF030099
	20	32	14.2	1353	6	AX201324
	21	32	14.2	1353	9	AY358870
	22	32	14.2	1368	9	AF055872
	23	32	14.2	1373	6	BD062758
	24	32	14.2	1421	6	BD090952
	25	32	14.2	1615	9	BC071837
	26	32	14.2	1642	9	BC019047
	27	32	14.2	1816	9	AY081051
c	28	32	14.2	60268	9	AC016876
	29	32	14.2	218485	2	AC127470
	30	30	13.3	148555	2	AC126921
	31	26	11.6	201	11	BV202888
	32	11	4.9	212093	2	AC126237
	33	11	4.9	346274	1	BX640443
	34	11	4.9	348014	1	BX640430
c	35	11	4.9	349672	1	BX640419
	36	10	4.4	9966	1	AE015249
	37	10	4.4	13606	1	AE005458
	38	10	4.4	15676	1	D90857
	39	10	4.4	18393	1	D90856
	40	10	4.4	110000	1	U00096_23
	41	10	4.4	191606	9	AL162376
c	42	10	4.4	254171	2	AC127182
c	43	10	4.4	287353	2	AC112589

44 10 4.4 292088 1 AE016986
45 10 4.4 296827 1 AP002561

AE016986 Shigella
AP002561 Escherich

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 17:01:58 ; Search time 452.373 Seconds
(without alignments)
2610.940 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 225

Sequence: 1 VLSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8266256

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162224_10195/app_query.fasta_1.7
82
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198_@CGN_1_1_586_@runat_20122004_162224_10195 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	225	100.0	1168	2	AAV18599	Aav18599 Mus muscu
2	225	100.0	1239	10	ADC97713	Adc97713 Murine FL
3	178	79.1	701	2	AAX23425	Aax23425 Mouse TNR
4	32	14.2	898	4	AAS03964	Aas03964 Expressio
5	32	14.2	1030	2	AAX23424	Aax23424 Human TNR
6	32	14.2	1236	2	AAV47613	Aav47613 TNF relat
7	32	14.2	1236	4	AAD04350	Aad04350 Human TRE
8	32	14.2	1306	8	ACC57901	Acc57901 Human TWE
9	32	14.2	1306	10	ADC35205	Adc35205 Human cDN
10	32	14.2	1306	10	AAD63914	Aad63914 Human TWE
11	32	14.2	1306	10	ACC57587	Acc57587 Polynucle
12	32	14.2	1353	3	AAA49717	Aaa49717 Human PRO
13	32	14.2	1353	6	ABK40255	Abk40255 cDNA enco
14	32	14.2	1353	10	ADJ37284	Adj37284 Human tum
15	32	14.2	1353	12	ADG68208	Adg68208 Human PRO
16	32	14.2	1364	6	ABK34881	Abk34881 Human cDN
17	32	14.2	1373	2	AAV18600	Aav18600 Homo sapi
18	32	14.2	1421	2	AAX56000	Aax56000 Human tum
19	10	4.4	408	8	ABX37032	Abx37032 Bovine ES
20	10	4.4	669	8	ACA19172	Aca19172 Prokaryot
c 21	9	4.0	149	2	AAQ33963	Aaq33963 Downstrea
22	9	4.0	434	6	ABZ08449	Abz08449 Human leu
c 23	9	4.0	562	5	AAF93579	Aaf93579 Lung carc
c 24	9	4.0	2494	10	ADA53039	Ada53039 Human cod
25	9	4.0	2990	4	ABL28781	Abl28781 Drosophil
c 26	9	4.0	3216	8	ABX34630	Abx34630 Human mdd
27	9	4.0	5637	4	ABL28780	Abl28780 Drosophil
c 28	8	3.6	24	2	AAX23452	Aax23452 Mouse TNR
c 29	8	3.6	24	2	AAX23451	Aax23451 Human TNR
c 30	8	3.6	232	5	AAH81829	Aah81829 Rat diffe
c 31	8	3.6	252	6	ABN20417	Abn20417 Human ORF
c 32	8	3.6	295	10	ABX88172	Abx88172 Corn ear-
c 33	8	3.6	302	10	ADF85713	Adf85713 Human ade
34	8	3.6	333	10	ADF03460	Adf03460 Bacterial
c 35	8	3.6	349	10	ADB55990	Adb55990 Toxicity-
c 36	8	3.6	351	6	ABL91276	Abl91276 Chlamydia
37	8	3.6	353	8	ABX46862	Abx46862 Bovine ES
38	8	3.6	369	8	ABX44905	Abx44905 Bovine ES
39	8	3.6	374	3	AAA31469	Aaa31469 Plant mic
40	8	3.6	380	3	AAA31422	Aaa31422 Plant mic
41	8	3.6	387	4	AAL01759	Aal01759 Human rep
42	8	3.6	387	4	ABL97052	Abl97052 Human tes
43	8	3.6	388	6	ABN63130	Abn63130 Human can
44	8	3.6	393	8	ACA38154	Aca38154 Prokaryot
c 45	8	3.6	396	8	ABX62757	Abx62757 Arabidops

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 21:13:13 ; Search time 80.6962 Seconds
(without alignments)
1981.847 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 225

Sequence: 1 VLSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1643610

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-
Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162225_10229/app_query.fasta_1.7
82
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=olip2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198@CGN_1_1_93@runat_20122004_162225_10229 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB		
	1	32	14.2	898	4	US-09-883-777-1	Sequence 1, Appli
	2	32	14.2	1236	3	US-09-105-343A-1	Sequence 1, Appli
	3	9	4.0	767	4	US-09-270-767-12088	Sequence 12088, A
c	4	8	3.6	35	4	US-09-724-566A-98	Sequence 98, Appli
c	5	8	3.6	295	4	US-09-313-294A-6632	Sequence 6632, Ap
	6	8	3.6	333	4	US-09-543-681A-3745	Sequence 3745, Ap
c	7	8	3.6	403	4	US-09-397-787-263	Sequence 263, App
	8	8	3.6	433	4	US-09-513-999C-1829	Sequence 1829, Ap
	9	8	3.6	537	4	US-09-252-991A-3995	Sequence 3995, Ap
	10	8	3.6	541	4	US-09-669-751-56	Sequence 56, Appli
	11	8	3.6	555	4	US-09-252-991A-11482	Sequence 11482, A
	12	8	3.6	584	4	US-09-232-785-315	Sequence 315, App
c	13	8	3.6	644	4	US-09-636-215-752	Sequence 752, App
c	14	8	3.6	644	4	US-09-685-166A-752	Sequence 752, App
c	15	8	3.6	644	4	US-09-679-426-752	Sequence 752, App
c	16	8	3.6	653	4	US-09-470-191-3	Sequence 3, Appli
c	17	8	3.6	810	4	US-09-248-796A-8173	Sequence 8173, Ap
c	18	8	3.6	852	4	US-09-252-991A-3914	Sequence 3914, Ap
	19	8	3.6	1069	4	US-09-270-767-14553	Sequence 14553, A
	20	8	3.6	1131	4	US-09-252-991A-11460	Sequence 11460, A
	21	8	3.6	1158	4	US-09-984-334-2	Sequence 2, Appli
c	22	8	3.6	1166	4	US-09-452-937A-33	Sequence 33, Appli
	23	8	3.6	1202	4	US-09-620-312D-97	Sequence 97, Appli
c	24	8	3.6	1272	4	US-09-252-991A-4557	Sequence 4557, Ap
c	25	8	3.6	1276	4	US-09-023-655-1091	Sequence 1091, Ap
c	26	8	3.6	1287	4	US-09-548-372D-50	Sequence 50, Appli
c	27	8	3.6	1287	4	US-09-548-367D-50	Sequence 50, Appli
c	28	8	3.6	1287	4	US-09-551-853D-50	Sequence 50, Appli
c	29	8	3.6	1287	4	US-09-416-901B-50	Sequence 50, Appli
c	30	8	3.6	1287	4	US-09-548-376D-50	Sequence 50, Appli
c	31	8	3.6	1287	4	US-09-794-927A-50	Sequence 50, Appli
c	32	8	3.6	1287	4	US-09-548-373D-50	Sequence 50, Appli
c	33	8	3.6	1287	4	US-09-795-847B-50	Sequence 50, Appli
c	34	8	3.6	1287	4	US-09-869-414-50	Sequence 50, Appli
c	35	8	3.6	1287	4	US-09-548-366F-50	Sequence 50, Appli
c	36	8	3.6	1302	4	US-09-548-372D-25	Sequence 25, Appli
c	37	8	3.6	1302	4	US-09-548-367D-25	Sequence 25, Appli
c	38	8	3.6	1302	4	US-09-551-853D-25	Sequence 25, Appli
c	39	8	3.6	1302	4	US-09-416-901B-25	Sequence 25, Appli
c	40	8	3.6	1302	4	US-09-548-376D-25	Sequence 25, Appli
c	41	8	3.6	1302	4	US-09-794-927A-25	Sequence 25, Appli
c	42	8	3.6	1302	4	US-09-548-373D-25	Sequence 25, Appli
c	43	8	3.6	1302	4	US-09-795-847B-25	Sequence 25, Appli
c	44	8	3.6	1302	4	US-09-869-414-25	Sequence 25, Appli
c	45	8	3.6	1302	4	US-09-548-366F-25	Sequence 25, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 21:10:13 ; Search time 3006.65 Seconds
(without alignments)
2726.939 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 225

Sequence: 1 VSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 1

Total number of hits satisfying chosen parameters: 65644295

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-
Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162224_10214/app_query.fasta_1.7
82
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198 @CGN_1_1_4385 @runat_20122004_162224_10214 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
	1	176	78.2	748	7	CN270781	CN270781 170005999
	2	160	71.1	2237	3	AK044387	AK044387 Mus muscu
	3	158	70.2	482	9	CG653257	CG653257 OST418407
	4	158	70.2	620	7	CK625052	CK625052 mi28e10.y
	5	143	63.6	665	6	BY742288	BY742288 BY742288
	6	143	63.6	1033	3	AK020909	AK020909 Mus muscu
	7	133	59.1	790	7	CO559990	CO559990 AGENCOURT
	8	131	58.2	939	6	CB849011	CB849011 MRA-0673
	9	129	57.3	584	2	AW917574	AW917574 EST348878
	10	128	56.9	561	2	AW763237	AW763237 ur70d09.y
	11	127	56.4	760	7	CO572381	CO572381 AGENCOURT
	12	123	54.7	892	6	CB204861	CB204861 AGENCOURT
	13	119	52.9	360	2	BE654876	BE654876 UI-M-BH0-
	14	118	52.4	918	2	BF577781	BF577781 602092080
	15	117	52.0	494	9	CG596702	CG596702 OST259234
	16	117	52.0	543	9	CG565104	CG565104 OST189654
	17	115	51.1	349	6	BY766420	BY766420 BY766420
	18	110	48.9	445	1	AA870722	AA870722 vq25g07.r
	19	109	48.4	692	6	BY748962	BY748962 BY748962
c	20	102	45.3	315	2	BF466521	BF466521 UI-M-CG0p
	21	98	43.6	531	9	CG590009	CG590009 OST242925
	22	97	43.1	471	1	AA221610	AA221610 my18d09.r
	23	97	43.1	650	4	BG404836	BG404836 602420160
	24	86	38.2	393	9	CG493044	CG493044 OST31172
	25	84	37.3	474	4	BI965174	BI965174 id34e07.y
	26	84	37.3	778	6	CB572618	CB572618 AGENCOURT
	27	80	35.6	581	4	BI738634	BI738634 603358846
	28	78	34.7	424	9	CG593688	CG593688 OST251087
	29	77	34.2	269	9	CG564287	CG564287 OST188290
	30	76	33.8	424	9	CG512379	CG512379 OST65281
	31	76	33.8	805	7	CO393621	CO393621 AGENCOURT
	32	74	32.9	554	9	CG629394	CG629394 OST341515
	33	70	31.1	774	7	CO574209	CO574209 AGENCOURT
	34	65	28.9	533	2	BE628951	BE628951 uu30c03.y
c	35	60	26.7	687	5	BQ208433	BQ208433 UI-R-EP0-
	36	58	25.8	493	2	BE307031	BE307031 601087888
	37	57	25.3	403	9	CG548201	CG548201 OST149561
	38	56	24.9	352	9	CG543056	CG543056 OST138358
	39	52	23.1	418	9	CG611020	CG611020 OST295426
	40	52	23.1	731	9	AG517989	AG517989 Mus muscu
c	41	51	22.7	487	2	AW320117	AW320117 un17b02.x
	42	48	21.3	342	1	AA637970	AA637970 vr30a10.r
	43	46	20.4	558	4	BM484863	BM484863 538865 MA
	44	45	20.0	621	9	CG584545	CG584545 OST230701
c	45	43	19.1	776	9	AG477136	AG477136 Mus muscu

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 16:43:23 ; Search time 4057.12 Seconds
(without alignments)
2622.595 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 1162

Sequence: 1 VSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-

Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162203_9562/app_query.fasta_1.78
2
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198@CGN_1_1_4236@runat_20122004_162203_9562 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

```

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1162	100.0	1168	6	BD062757	BD062757 A tumor n
2	1162	100.0	1239	10	AF030100	AF030100 Mus muscu
3	1134	97.6	1576	10	BC079107	BC079107 Rattus no
4	1126	96.9	750	10	AY607588	AY607588 Rattus no
5	1020	87.8	1236	6	AR140407	AR140407 Sequence
6	1020	87.8	1236	6	BD057124	BD057124 Member of
7	1020	87.8	1306	9	AF030099	AF030099 Homo sapi
8	1020	87.8	1353	6	AX201324	AX201324 Sequence
9	1020	87.8	1353	9	AY358870	AY358870 Homo sapi
10	1020	87.8	1368	9	AF055872	AF055872 Homo sapi
11	1020	87.8	1373	6	BD062758	BD062758 A tumor n
12	1020	87.8	1421	6	BD090952	BD090952 Apo-3 lig
13	951	81.8	898	6	AX180714	AX180714 Sequence
14	945.5	81.4	1615	9	BC071837	BC071837 Homo sapi
15	945.5	81.4	1642	9	BC019047	BC019047 Homo sapi
16	618.5	53.2	130254	2	AC136195	AC136195 Rattus no
c 17	618.5	53.2	165316	2	AC119115	AC119115 Rattus no
18	618.5	53.2	223877	2	AC098923	AC098923 Rattus no
c 19	618.5	53.2	225077	2	AC136563	AC136563 Rattus no
c 20	618.5	53.2	234801	2	AC118309	AC118309 Rattus no
21	613	52.8	1816	9	AY081051	AY081051 Homo sapi
c 22	602.5	51.9	203083	2	AC069459	AC069459 Mus muscu
c 23	602.5	51.9	234182	10	AL603707	AL603707 Mouse DNA
24	564.5	48.6	149736	2	AC126239	AC126239 Felis cat
25	550	47.3	180222	2	AC130192	AC130192 Sus scrof
c 26	549.5	47.3	60268	9	AC016876	AC016876 Homo sapi
27	549.5	47.3	218485	2	AC127470	AC127470 Pan trogl
28	544.5	46.9	176258	2	AC126925	AC126925 Canis fam
29	503	43.3	148555	2	AC126921	AC126921 Bos tauru
30	329	28.3	751	11	BV166827	BV166827 TNFSF12_2
31	207	17.8	212093	2	AC126237	AC126237 Canis fam
c 32	144	12.4	170189	2	BX957358	BX957358 Danio rer
33	144	12.4	237644	2	CR318653	CR318653 Danio rer
34	142	12.2	201	11	BV202888	BV202888 sqnm21025
c 35	121.5	10.5	302101	1	AE016784	AE016784 Pseudomon
36	117	10.1	1950	3	AK116689	AK116689 Ciona int
37	116.5	10.0	2165	3	BT001838	BT001838 Drosophil
38	113.5	9.8	1656	3	AB073865	AB073865 Drosophil
39	113.5	9.8	2101	3	AF149799	AF149799 Drosophil
40	110.5	9.5	978	6	CQ601692	CQ601692 Sequence
41	110.5	9.5	1221	3	AY119233	AY119233 Drosophil
42	110.5	9.5	1248	3	AY115551	AY115551 Drosophil
43	110.5	9.5	2159	3	AF521176	AF521176 Drosophil

c 44 109.5 9.4 108967 9 AL353138
c 45 109 9.4 166863 2 AC150140

AL353138 Human DNA
AC150140 Gallus ga

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 16:40:38 ; Search time 452.848 Seconds
(without alignments)
2608.203 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 1162

Sequence: 1 VLSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-

Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162203_9545/app_query.fasta_1.78
2
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198@CGN_1_1_586@runat_20122004_162203_9545 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1162	100.0	1168	2	AAV18599	Aav18599 Mus muscu
2	1162	100.0	1239	10	ADC97713	Adc97713 Murine FL
3	1089	93.7	701	2	AAX23425	Aax23425 Mouse TNR
4	1020	87.8	1236	2	AAV47613	Aav47613 TNF relat
5	1020	87.8	1236	4	AAD04350	Aad04350 Human TRE
6	1020	87.8	1306	8	ACC57901	Acc57901 Human TWE
7	1020	87.8	1306	10	ADC35205	Adc35205 Human cDN
8	1020	87.8	1306	10	AAD63914	Aad63914 Human TWE
9	1020	87.8	1306	10	ACC57587	Acc57587 Polynucle
10	1020	87.8	1353	3	AAA49717	Aaa49717 Human PRO
11	1020	87.8	1353	6	ABK40255	Abk40255 cDNA enco
12	1020	87.8	1353	10	ADJ37284	Adj37284 Human tum
13	1020	87.8	1353	12	ADG68208	Adg68208 Human PRO
14	1020	87.8	1364	6	ABK34881	Abk34881 Human cDN
15	1020	87.8	1373	2	AAV18600	Aav18600 Homo sapi
16	1020	87.8	1421	2	AAX56000	Aax56000 Human tum
17	951	81.8	898	4	AAS03964	Aas03964 Expressio
18	951	81.8	1030	2	AAX23424	Aax23424 Human TNR
19	348	29.9	408	8	ABX37032	Abx37032 Bovine ES
20	121.5	10.5	1278	8	ACA43832	Aca43832 Prokaryot
21	113.5	9.8	2148	6	ABK11680	Abk11680 DNA encod
22	111	9.6	1221	6	ABK11679	Abk11679 DNA encod
23	110.5	9.5	978	4	ABL21473	Ab121473 Drosophil
24	109.5	9.4	1212	10	ADD29692	Add29692 Human tum
25	106.5	9.2	1630	2	AAV41377	Aav41377 NF-kB rec
26	106.5	9.2	1630	2	AAV41371	Aav41371 NF-kB rec
27	106.5	9.2	1630	2	AAD15310	Aad15310 Murine re
28	106.5	9.2	1630	4	AAD08714	Aad08714 Murine re
29	106.5	9.2	1630	4	AAD05903	Aad05903 Murine RA
30	106.5	9.2	1630	6	AAD43212	Aad43212 Mouse RAN
31	106.5	9.2	1630	9	ADB16985	Adb16985 Murine re
32	106.5	9.2	1630	10	ADC72999	Adc72999 Murine RA
33	106.5	9.2	1630	10	ADC78265	Adc78265 Murine RA
34	106.5	9.2	1630	10	ADG46720	Adg46720 Murine RA
35	106.5	9.2	3878	4	AAD05230	Aad05230 Human sec
36	106.5	9.2	3878	10	ADA56393	Ada56393 Gene enco
37	106.5	9.2	4034	4	AAH93868	Aah93868 P553S cDN
38	106.5	9.2	4034	4	AAS64040	Aas64040 Human pro
39	106.5	9.2	4034	5	ACA59848	Aca59848 Prostate
40	106.5	9.2	4034	6	ABL95411	Ab195411 Human P55
41	106.5	9.2	4034	8	ACC95575	Acc95575 Prostate
42	106.5	9.2	4034	10	ADB14154	Adb14154 Human pro
43	106.5	9.2	4034	10	ADG26570	Adg26570 Human pro
44	106.5	9.2	4894	4	AAH93866	Aah93866 P553S cDN
45	106.5	9.2	4894	4	AAS64038	Aas64038 Human pro

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 16:42:43 ; Search time 3007.12 Seconds
(without alignments)
2726.509 Million cell updates/sec

Title: US-09-245-198A-2

Perfect score: 1162

Sequence: 1 VLSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162203_9569/app_query.fasta_1.78
2
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198_@CGN_1_1_4385_@runat_20122004_162203_9569 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1104	95.0	790	7	CO559990	CO559990 AGENCOURT
2	1063.5	91.5	760	7	CO572381	CO572381 AGENCOURT
3	1039	89.4	918	2	BF577781	BF577781 602092080
4	968.5	83.3	731	4	BI871711	BI871711 603395825
5	954.5	82.1	2237	3	AK044387	AK044387 Mus muscu
6	941.5	81.0	728	4	BI870393	BI870393 603395641
7	936.5	80.6	620	7	CK625052	CK625052 mi28e10.y
8	920	79.2	748	7	CN270781	CN270781 170005999
9	916	78.8	805	7	CO393621	CO393621 AGENCOURT
10	882	75.9	777	4	BI819200	BI819200 603034614
11	875	75.3	666	6	CF126539	CF126539 UI-HF-ET0
12	864	74.4	545	6	CB141389	CB141389 K-EST0194
13	861	74.1	828	4	BI596681	BI596681 603243254
14	861	74.1	834	4	BI766766	BI766766 603056866
15	857	73.8	561	2	AW763237	AW763237 ur70d09.y
16	831.5	71.6	948	5	BQ707185	BQ707185 AGENCOURT
17	827	71.2	482	9	CG653257	CG653257 OST418407
18	820	70.6	774	7	CO574209	CO574209 AGENCOURT
19	818	70.4	940	5	BQ884231	BQ884231 AGENCOURT
20	797	68.6	543	9	CG565104	CG565104 OST189654
21	789.5	67.9	697	6	CF126932	CF126932 UI-HF-ET0
22	764	65.7	963	5	BQ671259	BQ671259 AGENCOURT
23	754	64.9	665	6	BY742288	BY742288 BY742288
24	754	64.9	1033	3	AK020909	AK020909 Mus muscu
25	731	62.9	498	9	CG554711	CG554711 OST168603
26	721	62.0	1071	4	BM921213	BM921213 AGENCOURT
27	709.5	61.1	474	9	CG609156	CG609156 OST290052
28	703	60.5	951	5	BQ674188	BQ674188 AGENCOURT
29	699.5	60.2	621	9	CG584545	CG584545 OST230701
30	699	60.2	584	2	AW917574	AW917574 EST348878
31	697	60.0	939	6	CB849011	CB849011 MRA-0673
32	696	59.9	483	9	CG646715	CG646715 OST393421
33	677	58.3	418	9	CG611020	CG611020 OST295426
34	670	57.7	445	1	AA870722	AA870722 vq25g07.r
35	665.5	57.3	531	9	CG590009	CG590009 OST242925
36	662	57.0	471	9	CG568080	CG568080 OST194813
37	654	56.3	494	9	CG596702	CG596702 OST259234
38	648	55.8	567	6	CA396679	CA396679 cs80h07.y
39	645	55.5	892	6	CB204861	CB204861 AGENCOURT
40	644.5	55.5	704	7	CK357507	CK357507 AGENCOURT
41	633	54.5	554	9	CG629394	CG629394 OST341515
42	632.5	54.4	471	1	AA221610	AA221610 my18d09.r
43	629	54.1	650	4	BG404836	BG404836 602420160
44	621	53.4	360	2	BE654876	BE654876 UI-M-BH0-
45	610	52.5	785	4	BI762908	BI762908 603047966

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:48:53 ; Search time 3514 Seconds
(without alignments)
10052.762 Million cell updates/sec

Title: US-09-245-198A-3_COPY_106_852
Perfect score: 747
Sequence: 1 atggccgcccgtcggagcca.....tcggactcttccaggttcac 747

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
1	747	100.0	1306	9	AF030099	AF030099 Homo sapi
2	747	100.0	1373	6	BD062758	BD062758 A tumor n
3	696	93.2	1353	6	AX201324	AX201324 Sequence

4	696	93.2	1353	9	AY358870	AY358870 Homo sapi	
5	696	93.2	1368	9	AF055872	AF055872 Homo sapi	
6	696	93.2	1421	6	BD090952	BD090952 Apo-3 lig	
7	622	83.3	1236	6	AR140407	AR140407 Sequence	
8	622	83.3	1236	6	BD057124	BD057124 Member of	
9	621	83.1	898	6	AX180714	AX180714 Sequence	
10	498	66.7	1816	9	AY081051	AY081051 Homo sapi	
11	377	50.5	1615	9	BC071837	BC071837 Homo sapi	
12	373	49.9	1642	9	BC019047	BC019047 Homo sapi	
13	201	26.9	218485	2	AC127470	AC127470 Pan trogl	
c	14	160	21.4	60268	9	AC016876	AC016876 Homo sapi
	15	80	10.7	201	11	BV202888	BV202888 sqnm21025
	16	72	9.6	751	11	BV166827	BV166827 TNFSF12_2
	17	64	8.6	750	10	AY607588	AY607588 Rattus no
	18	64	8.6	1239	10	AF030100	AF030100 Mus muscu
	19	64	8.6	1576	10	BC079107	BC079107 Rattus no
	20	64	8.6	130254	2	AC136195	AC136195 Rattus no
c	21	64	8.6	165316	2	AC119115	AC119115 Rattus no
	22	64	8.6	180222	2	AC130192	AC130192 Sus scrof
c	23	64	8.6	203083	2	AC069459	AC069459 Mus muscu
	24	64	8.6	223877	2	AC098923	AC098923 Rattus no
c	25	64	8.6	225077	2	AC136563	AC136563 Rattus no
	26	64	8.6	234182	10	AL603707	AL603707 Mouse DNA
c	27	58	7.8	148555	2	AC126921	AC126921 Bos tauru
	28	58	7.8	176258	2	AC126925	AC126925 Canis fam
	29	53	7.1	149736	2	AC126239	AC126239 Felis cat
	30	50	6.7	50	6	AX201395	AX201395 Sequence
	31	50	6.7	50	6	BD090954	BD090954 Apo-3 lig
	32	46	6.2	1168	6	BD062757	BD062757 A tumor n
	33	44	5.9	212093	2	AC126237	AC126237 Canis fam
	34	31	4.1	234801	2	AC118309	AC118309 Rattus no
	35	24	3.2	40	6	BD090955	BD090955 Apo-3 lig
	36	22	2.9	1005	6	AX695886	AX695886 Sequence
c	37	22	2.9	1173	1	AF182516	AF182516 Pseudomon
	38	22	2.9	2942	6	AX695885	AX695885 Sequence
	39	22	2.9	2942	10	MMU250723	AJ250723 Mus muscu
	40	22	2.9	3579	10	AK122415	AK122415 Mus muscu
	41	22	2.9	3642	10	BC046524	BC046524 Mus muscu
	42	22	2.9	10989	10	AF450138S4	AF450141 Mus muscu
	43	22	2.9	50295	6	AX695884	AX695884 Sequence
	44	22	2.9	136916	8	AC133398	AC133398 Oryza sat
	45	22	2.9	209068	10	AL603868	AL603868 Mouse DNA

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:22:53 ; Search time 477 Seconds
(without alignments)
8220.791 Million cell updates/sec

Title: US-09-245-198A-3_COPY_106_852
Perfect score: 747
Sequence: 1 atggccgcccgtcggagcca.....tcggactcttccaggttcac 747

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	747	100.0	1306	8	ACC57901	Acc57901 Human TWE
2	747	100.0	1306	10	ADC35205	Adc35205 Human cDN
3	747	100.0	1306	10	AAD63914	Aad63914 Human TWE
4	747	100.0	1306	10	ACC57587	Acc57587 Polynucle
5	747	100.0	1373	2	AAV18600	Aav18600 Homo sapi
6	696	93.2	1353	3	AAA49717	Aaa49717 Human PRO

7	696	93.2	1353	6	ABK40255	Abk40255 cDNA enco
8	696	93.2	1353	10	ADJ37284	Adj37284 Human tum
9	696	93.2	1353	12	ADG68208	Adg68208 Human PRO
10	696	93.2	1364	6	ABK34881	Abk34881 Human cDN
11	696	93.2	1421	2	AAX56000	Aax56000 Human tum
12	622	83.3	1236	2	AAV47613	Aav47613 TNF relat
13	622	83.3	1236	4	AAD04350	Aad04350 Human TRE
14	621	83.1	898	4	AAS03964	Aas03964 Expressio
15	573	76.7	1030	2	AAX23424	Aax23424 Human TNR
16	64	8.6	1239	10	ADC97713	Adc97713 Murine FL
17	50	6.7	50	2	AAX56002	Aax56002 Human tum
18	50	6.7	50	3	AAA49732	Aaa49732 Human PRO
19	50	6.7	50	6	ABK40292	Abk40292 Oligonucl
20	50	6.7	50	10	ADJ37355	Adj37355 Tumour th
21	50	6.7	50	12	ADG68279	Adg68279 Human PRO
22	46	6.2	701	2	AAX23425	Aax23425 Mouse TNR
23	46	6.2	1168	2	AAV18599	Aav18599 Mus muscu
24	36	4.8	408	8	ABX37032	Abx37032 Bovine ES
c 25	24	3.2	24	2	AAX23451	Aax23451 Human TNR
c 26	24	3.2	24	2	AAX23450	Aax23450 Human TNR
27	24	3.2	40	2	AAX56003	Aax56003 Human tum
28	22	2.9	1005	9	ADA02995	Ada02995 Mouse Sep
29	22	2.9	1005	10	ADB72733	Adb72733 Mouse Sep
30	22	2.9	1005	10	ADC85475	Adc85475 Mouse Sep
31	22	2.9	1005	12	ADM74590	Adm74590 Murine ca
32	22	2.9	2942	9	ADA02994	Ada02994 Mouse Sep
33	22	2.9	2942	10	ADB72732	Adb72732 Mouse Sep
34	22	2.9	2942	10	ADC85474	Adc85474 Mouse Sep
35	22	2.9	2942	12	ADM74589	Adm74589 Murine ca
36	22	2.9	50295	9	ADA02993	Ada02993 Mouse Sep
37	22	2.9	50295	10	ADB72731	Adb72731 Mouse Sep
38	22	2.9	50295	10	ADC85473	Adc85473 Mouse Sep
39	22	2.9	50295	12	ADM74588	Adm74588 Murine ca
40	20	2.7	20	2	AAV18603	Aav18603 Synthetic
41	20	2.7	20	2	AAV18609	Aav18609 Synthetic
42	20	2.7	20	2	AAV18602	Aav18602 Synthetic
43	20	2.7	20	2	AAV18606	Aav18606 Synthetic
44	20	2.7	20	2	AAV18605	Aav18605 Synthetic
45	20	2.7	47	3	AAA49772	Aaa49772 Human PRO

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 10:49:48 ; Search time 3079 Seconds
(without alignments)
8840.688 Million cell updates/sec

Title: US-09-245-198A-3_COPY_106_852
Perfect score: 747
Sequence: 1 atggccgcccgtcggagcca.....tcggactcttcaggttcac 747

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description	
No.	Score	Match	Length	DB	ID	Description
1	544	72.8	545	6	CB141389	CB141389 K-EST0194
2	516	69.1	567	6	CA396679	CA396679 cs80h07.y
3	514	68.8	777	4	BI819200	BI819200 603034614
4	506	67.7	728	4	BI870393	BI870393 603395641
5	506	67.7	731	4	BI871711	BI871711 603395825
6	490	65.6	828	4	BI596681	BI596681 603243254
7	448	60.0	666	6	CF126539	CF126539 UI-HF-ET0
8	445	59.6	963	5	BQ671259	BQ671259 AGENCOURT
9	436	58.4	940	5	BQ884231	BQ884231 AGENCOURT

10	425	56.9	697	6	CF126932	CF126932 UI-HF-ET0	
11	390	52.2	1071	4	BM921213	BM921213 AGENCOURT	
12	378	50.6	948	5	BQ707185	BQ707185 AGENCOURT	
13	376	50.3	834	4	BI766766	BI766766 603056866	
14	349	46.7	951	5	BQ674188	BQ674188 AGENCOURT	
15	308	41.2	824	6	CB998034	CB998034 AGENCOURT	
16	290	38.8	298	4	BM688946	BM688946 UI-E-CQ1-	
17	253	33.9	776	5	BX090012	BX090012 BX090012	
18	230	30.8	587	4	BG686319	BG686319 602638232	
19	217	29.0	698	4	BI906850	BI906850 603064633	
20	206	27.6	894	4	BI908274	BI908274 603068526	
21	159	21.3	1064	7	CF994566	CF994566 AGENCOURT	
22	159	21.3	1319	7	CF594233	CF594233 AGENCOURT	
23	147	19.7	456	4	BI966255	BI966255 ie72g04.y	
24	141	18.9	910	4	BG110063	BG110063 602279667	
25	132	17.7	785	4	BI762908	BI762908 603047966	
26	121	16.2	465	1	AI091441	AI091441 ow62g05.x	
27	114	15.3	345	7	R55379	R55379 yj77a08.r1	
28	91	12.2	1187	5	BQ053284	BQ053284 AGENCOURT	
29	86	11.5	531	4	BI824443	BI824443 603038693	
30	86	11.5	538	2	BF821434	BF821434 MR1-RT003	
31	79	10.6	837	6	CB961075	CB961075 AGENCOURT	
32	77	10.3	367	8	AQ100365	AQ100365 HS_3054_A	
33	73	9.8	278	2	AW417023	AW417023 52923 MAR	
34	73	9.8	404	2	BF044430	BF044430 BP250013A	
35	73	9.8	542	2	BF041509	BF041509 BP250025B	
c	36	73	9.8	808	7	CK769182	CK769182 956712 MA
c	37	66	8.8	609	4	BI966060	BI966060 ie72g04.x
	38	64	8.6	474	4	BI965174	BI965174 id34e07.y
	39	64	8.6	639	2	BB642326	BB642326 BB642326
	40	64	8.6	692	6	BY748962	BY748962 BY748962
	41	64	8.6	704	7	CK357507	CK357507 AGENCOURT
	42	64	8.6	741	7	CO398911	CO398911 AGENCOURT
	43	64	8.6	774	7	CO574209	CO574209 AGENCOURT
	44	64	8.6	862	5	BP173436	BP173436 BP173436
	45	64	8.6	2237	3	AK044387	AK044387 Mus muscu

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 03:07:38 ; Search time 3413.97 Seconds
(without alignments)
10347.323 Million cell updates/sec

Title: US-09-245-198A-3_COPY_106_852
Perfect score: 747
Sequence: 1 atggccgcccgtcggagcca.....tcggactttccaggttcac 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	747	100.0	1306	9	AF030099	AF030099 Homo sapi
2	747	100.0	1373	6	BD062758	BD062758 A tumor n
3	745.4	99.8	1353	6	AX201324	AX201324 Sequence

4	745.4	99.8	1353	9	AY358870	AY358870 Homo sapi	
5	745.4	99.8	1368	9	AF055872	AF055872 Homo sapi	
6	745.4	99.8	1421	6	BD090952	BD090952 Apo-3 lig	
7	742.2	99.4	1236	6	AR140407	AR140407 Sequence	
8	742.2	99.4	1236	6	BD057124	BD057124 Member of	
9	621	83.1	898	6	AX180714	AX180714 Sequence	
10	607.8	81.4	1239	10	AF030100	AF030100 Mus muscu	
11	606.2	81.2	750	10	AY607588	AY607588 Rattus no	
12	604.6	80.9	1576	10	BC079107	BC079107 Rattus no	
13	539	72.2	1168	6	BD062757	BD062757 A tumor n	
14	498	66.7	1615	9	BC071837	BC071837 Homo sapi	
15	498	66.7	1816	9	AY081051	AY081051 Homo sapi	
16	496.4	66.5	1642	9	BC019047	BC019047 Homo sapi	
17	250.4	33.5	218485	2	AC127470	AC127470 Pan trogl	
c	18	248.8	33.3	60268	9	AC016876	AC016876 Homo sapi
	19	225.2	30.1	180222	2	AC130192	AC130192 Sus scrof
	20	220.4	29.5	148555	2	AC126921	AC126921 Bos tauru
	21	218.4	29.2	176258	2	AC126925	AC126925 Canis fam
	22	215.8	28.9	149736	2	AC126239	AC126239 Felis cat
c	23	215.2	28.8	130254	2	AC136195	AC136195 Rattus no
	24	215.2	28.8	165316	2	AC119115	AC119115 Rattus no
	25	215.2	28.8	223877	2	AC098923	AC098923 Rattus no
	26	215.2	28.8	225077	2	AC136563	AC136563 Rattus no
	27	215.2	28.8	234801	2	AC118309	AC118309 Rattus no
c	28	213.6	28.6	203083	2	AC069459	AC069459 Mus muscu
c	29	213.6	28.6	234182	10	AL603707	AL603707 Mouse DNA
	30	196.4	26.3	751	11	BV166827	BV166827 TNFSF12_2
	31	146.6	19.6	212093	2	AC126237	AC126237 Canis fam
	32	80	10.7	201	11	BV202888	BV202888 sqnm21025
c	33	57	7.6	125020	9	AF429315	AF429315 Homo sapi
c	34	56.8	7.6	125020	9	AF429315	AF429315 Homo sapi
c	35	53.4	7.1	280558	1	AE017301	AE017301 Thermus t
c	36	52.8	7.1	309050	1	SCO939117	AL939117 Streptomy
c	37	52.6	7.0	346362	1	BX640439	BX640439 Bordetell
c	38	52.2	7.0	1094	11	PM7G11B	AL685196 Penicilli
c	39	52.2	7.0	348257	1	BX640425	BX640425 Bordetell
c	40	52	7.0	3718	1	AF005842	AF005842 Rhodobact
c	41	51.6	6.9	2733	10	AY158896	AY158896 Rattus no
c	42	51.6	6.9	166614	2	AC141334	AC141334 Rattus no
c	43	51.6	6.9	205793	2	AC126989	AC126989 Rattus no
c	44	51.6	6.9	277424	2	AC120729	AC120729 Rattus no
c	45	51.2	6.9	2336	6	AX748400	AX748400 Sequence

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OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 23:41:48 ; Search time 424.405 Seconds
(without alignments)
9239.560 Million cell updates/sec

Title: US-09-245-198A-3_COPY_106_852
Perfect score: 747
Sequence: 1 atggccgcccgtcggagcca.....tcggactcttcaggttcac 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	747	100.0	1306	8	ACC57901	Acc57901 Human TWE
2	747	100.0	1306	10	ADC35205	Adc35205 Human cDN
3	747	100.0	1306	10	AAD63914	Aad63914 Human TWE
4	747	100.0	1306	10	ACC57587	Acc57587 Polynucle
5	747	100.0	1373	2	AAV18600	Aav18600 Homo sapi
6	745.4	99.8	1353	3	AAA49717	Aaa49717 Human PRO

7	745.4	99.8	1353	6	ABK40255	Abk40255 cDNA enco	
8	745.4	99.8	1353	10	ADJ37284	Adj37284 Human tum	
9	745.4	99.8	1353	12	ADG68208	Adg68208 Human PRO	
10	745.4	99.8	1364	6	ABK34881	Abk34881 Human cDN	
11	745.4	99.8	1421	2	AAX56000	Aax56000 Human tum	
12	742.2	99.4	1236	2	AAV47613	Aav47613 TNF relat	
13	742.2	99.4	1236	4	AAD04350	Aad04350 Human TRE	
14	622.4	83.3	1030	2	AAX23424	Aax23424 Human TNR	
15	621	83.1	898	4	AAS03964	Aas03964 Expressio	
16	607.8	81.4	1239	10	ADC97713	Adc97713 Murine FL	
17	539	72.2	1168	2	AAV18599	Aav18599 Mus muscu	
18	503.4	67.4	701	2	AAX23425	Aax23425 Mouse TNR	
19	273.6	36.6	408	8	ABX37032	Abx37032 Bovine ES	
20	91.4	12.2	264	8	ABX52254	Abx52254 Bovine ES	
21	51.6	6.9	2733	12	ADG98280	Adg98280 Rat CLG g	
22	51.2	6.9	2336	10	ADB63771	Adb63771 Human cDN	
23	50	6.7	50	2	AAX56002	Aax56002 Human tum	
24	50	6.7	50	3	AAA49732	Aaa49732 Human PRO	
25	50	6.7	50	6	ABK40292	Abk40292 Oligonucl	
26	50	6.7	50	10	ADJ37355	Adj37355 Tumour th	
27	50	6.7	50	12	ADG68279	Adg68279 Human PRO	
28	50	6.7	1608	6	AAD41201	Aad41201 Human nuc	
c	29	48.6	6.5	1077	8	ACA37803	Aca37803 Prokaryot
	30	48.4	6.5	2000	8	ADA71938	Ada71938 Rice gene
c	31	47.8	6.4	114955	2	AAX53491	Aax53491 Human ade
	32	47.4	6.3	2456	6	AAD42268	Aad42268 Human ELG
	33	46.8	6.3	1461	11	ABD16672	Abd16672 Pseudomon
	34	46.8	6.3	1578	11	ABD16771	Abd16771 Pseudomon
c	35	46.8	6.3	1608	11	ABD16798	Abd16798 Pseudomon
	36	46.8	6.3	13987	2	AAT80415	Aat80415 Hybrid sr
	37	46.8	6.3	44377	2	AAT80414	Aat80414 Platenoli
	38	46.8	6.3	44377	2	AAT78508	Aat78508 Platenoli
	39	46.6	6.2	609	11	ABD05820	Abd05820 Pseudomon
	40	46.6	6.2	789	11	ABD06021	Abd06021 Pseudomon
	41	46.6	6.2	840	11	ABD05923	Abd05923 Pseudomon
c	42	46.6	6.2	1164	11	ABD05645	Abd05645 Pseudomon
	43	46.2	6.2	754	8	ACA27025	Aca27025 Prokaryot
	44	45.8	6.1	645	3	AAZ24699	Aaz24699 Delayed r
	45	45.8	6.1	1252	6	ABZ35552	Abz35552 Human gen

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:35:48 ; Search time 2829.24 Seconds
(without alignments)
9621.134 Million cell updates/sec

Title: US-09-245-198A-3_COPY_106_852
Perfect score: 747
Sequence: 1 atggccgcccgtcggagcca.....tcggactcttccaggttcac 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	636	85.1	731	4	BI871711	BI871711 603395825
2	624	83.5	728	4	BI870393	BI870393 603395641
3	611.4	81.8	697	6	CF126932	CF126932 UI-HF-ET0
4	563.4	75.4	777	4	BI819200	BI819200 603034614
5	558	74.7	834	4	BI766766	BI766766 603056866
6	556.2	74.5	666	6	CF126539	CF126539 UI-HF-ET0
7	544	72.8	545	6	CB141389	CB141389 K-EST0194
8	539.4	72.2	828	4	BI596681	BI596681 603243254
9	527.4	70.6	948	5	BQ707185	BQ707185 AGENCOURT

10	520	69.6	790	7	CO559990	CO559990 AGENCOURT
11	516	69.1	567	6	CA396679	CA396679 cs80h07.y
12	504.8	67.6	940	5	BQ884231	BQ884231 AGENCOURT
13	498.4	66.7	805	7	CO393621	CO393621 AGENCOURT
14	496.8	66.5	2237	3	AK044387	AK044387 Mus muscu
15	493.2	66.0	760	7	CO572381	CO572381 AGENCOURT
16	484.6	64.9	918	2	BF577781	BF577781 602092080
17	480.8	64.4	620	7	CK625052	CK625052 mi28e10.y
18	472	63.2	963	5	BQ671259	BQ671259 AGENCOURT
19	458	61.3	774	7	CO574209	CO574209 AGENCOURT
20	454.4	60.8	561	2	AW763237	AW763237 ur70d09.y
21	439.4	58.8	1071	4	BM921213	BM921213 AGENCOURT
22	436.4	58.4	951	5	BQ674188	BQ674188 AGENCOURT
23	429.2	57.5	748	7	CN270781	CN270781 170005999
24	414.8	55.5	824	6	CB998034	CB998034 AGENCOURT
25	388.8	52.0	785	4	BI762908	BI762908 603047966
26	378.8	50.7	543	9	CG565104	CG565104 OST189654
27	371.4	49.7	704	7	CK357507	CK357507 AGENCOURT
28	370.4	49.6	482	9	CG653257	CG653257 OST418407
29	365	48.9	1064	7	CF994566	CF994566 AGENCOURT
30	361.8	48.4	587	4	BG686319	BG686319 602638232
31	361.2	48.4	665	6	BY742288	BY742288 BY742288
32	361.2	48.4	1033	3	AK020909	AK020909 Mus muscu
33	356.8	47.8	1319	7	CF594233	CF594233 AGENCOURT
34	352.4	47.2	498	9	CG554711	CG554711 OST168603
35	348.8	46.7	894	4	BI908274	BI908274 603068526
36	345.8	46.3	621	9	CG584545	CG584545 OST230701
37	338.4	45.3	584	2	AW917574	AW917574 EST348878
38	335.8	45.0	939	6	CB849011	CB849011 MRA-0673
39	332	44.4	474	9	CG609156	CG609156 OST290052
40	331.2	44.3	698	4	BI906850	BI906850 603064633
41	320.8	42.9	483	9	CG646715	CG646715 OST393421
42	320.4	42.9	418	9	CG611020	CG611020 OST295426
43	318.2	42.6	741	7	CO398911	CO398911 AGENCOURT
44	318	42.6	542	2	BF041509	BF041509 BP250025B
45	315.8	42.3	692	6	BY748962	BY748962 BY748962

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OM protein - protein search, using sw model

Run on: December 21, 2004, 16:26:57 ; Search time 57.7848 Seconds
(without alignments)
1545.797 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284
Perfect score: 249
Sequence: 1 MAARRSQRRGRRGEPGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	249	100.0	249	2	AAY09369	Aay09369 Human tum
2	249	100.0	249	3	AAY95338	Aay95338 Human PRO
3	249	100.0	249	3	AAB07526	Aab07526 Amino aci
4	249	100.0	249	5	AAU86129	Aau86129 Human PRO
5	249	100.0	249	6	ABR42315	Abr42315 Human TWE
6	249	100.0	249	7	ADC35206	Adc35206 Human TNF
7	249	100.0	249	7	ABW02278	Abw02278 Human TWE
8	249	100.0	249	7	ADJ37285	Adj37285 Human tum
9	249	100.0	249	8	ADG68209	Adg68209 Human PRO

10	249	100.0	284	2	AAW47525	Aaw47525 Homo sapi
11	241	96.8	249	2	AAW29745	Aaw29745 TNF relat
12	241	96.8	249	4	AAE00891	Aae00891 Human TRE
13	207	83.1	273	4	AAU03499	Aau03499 TWEAK ext
14	146	58.6	146	4	AAE00895	Aae00895 Human TRE
15	143	57.4	189	2	AAW29746	Aaw29746 TNF relat
16	143	57.4	189	4	AAE00892	Aae00892 Human UL4
17	107	43.0	208	2	AAW93590	Aaw93590 Human TNR
18	46	18.5	211	2	AAW93591	Aaw93591 Mouse TNR
19	32	12.9	225	2	AAW47524	Aaw47524 Mus muscu
20	32	12.9	225	3	AAB07527	Aab07527 Amino aci
21	32	12.9	249	7	ADC97712	Adc97712 Murine FL
22	9	3.6	138	7	ABO72203	Abo72203 Pseudomon
23	9	3.6	365	6	ABR41235	Abr41235 Human DIT
24	9	3.6	748	2	AAY14906	Aay14906 Extended
25	9	3.6	749	5	ABB73512	Abb73512 M vaccae
26	8	3.2	55	4	AAM20858	Aam20858 Peptide #
27	8	3.2	55	4	ABB42637	Abb42637 Peptide #
28	8	3.2	55	4	AAM36451	Aam36451 Peptide #
29	8	3.2	55	4	ABB25983	Abb25983 Protein #
30	8	3.2	55	4	AAM76342	Aam76342 Human bon
31	8	3.2	55	4	AAM63528	Aam63528 Human bra
32	8	3.2	55	4	ABG58050	Abg58050 Human liv
33	8	3.2	55	5	ABG45635	Abg45635 Human pep
34	8	3.2	65	4	AAM21621	Aam21621 Peptide #
35	8	3.2	65	4	ABB43981	Abb43981 Peptide #
36	8	3.2	65	4	AAM37923	Aam37923 Peptide #
37	8	3.2	65	4	ABB26890	Abb26890 Protein #
38	8	3.2	65	4	AAM77706	Aam77706 Human bon
39	8	3.2	65	4	AAM64984	Aam64984 Human bra
40	8	3.2	65	4	ABG59361	Abg59361 Human liv
41	8	3.2	65	5	ABG46737	Abg46737 Human pep
42	8	3.2	69	4	ABG03723	Abg03723 Novel hum
43	8	3.2	71	4	ABG03663	Abg03663 Novel hum
44	8	3.2	84	4	AAU61282	Aau61282 Propionib
45	8	3.2	84	6	ABM57801	Abm57801 Propionib

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OM protein - protein search, using sw model

Run on: December 21, 2004, 16:29:37 ; Search time 15.7595 Seconds
(without alignments)
1520.225 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284
Perfect score: 249
Sequence: 1 MAARRSQRRRGRRGEPEGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	10	4.0	111	2	A85866	hypothetical prote
2	9	3.6	733	2	S78376	photosystem I P700
3	8	3.2	58	2	A58208	protamine I-1 - pa
4	8	3.2	143	2	G84168	hypothetical prote
5	8	3.2	220	2	AG3547	bicyclomycin resis
6	8	3.2	278	2	D83080	hypothetical prote
7	8	3.2	339	2	C71132	hypothetical prote
8	8	3.2	372	2	H70813	probable cysteine
9	8	3.2	379	2	E64300	formate dehydrogen
10	8	3.2	381	2	AH3041	conserved hypothet
11	8	3.2	387	2	D84885	hypothetical prote
12	8	3.2	397	2	D98244	hypothetical prote
13	8	3.2	422	1	A60503	sperm-binding glyc
14	8	3.2	443	2	T17220	hypothetical prote

15	8	3.2	465	2	AC0347	probable membrane
16	8	3.2	471	2	A75267	probable transport
17	8	3.2	576	2	E64186	probable ATP-bindin
18	8	3.2	586	2	A41125	gamma-glutamyltran
19	7	2.8	45	2	D58208	protamine II-3 - p
20	7	2.8	50	2	S22582	protamine 1 - Sagu
21	7	2.8	58	2	S34045	protamine - North
22	7	2.8	86	2	F87604	hypothetical prote
23	7	2.8	102	2	F87993	protein ZC334.3 [i
24	7	2.8	115	2	PH1560	Ig heavy chain V r
25	7	2.8	115	2	H83201	conserved hypothet
26	7	2.8	125	2	T27519	hypothetical prote
27	7	2.8	131	2	E30552	T-cell activation
28	7	2.8	131	2	I52290	interleukin-13 - r
29	7	2.8	146	2	T37116	probable transposa
30	7	2.8	147	2	A71217	hypothetical prote
31	7	2.8	150	2	T08734	hypothetical prote
32	7	2.8	157	2	T02664	allergen - rice
33	7	2.8	157	2	S31078	seed allergen RA5
34	7	2.8	157	2	A75567	conserved hypothet
35	7	2.8	157	2	E75530	hypothetical prote
36	7	2.8	160	2	S59925	allergen RA5B prec
37	7	2.8	161	1	DNEC17	outer membrane pro
38	7	2.8	161	2	D90651	histone-like prote
39	7	2.8	161	2	D85502	hypothetical prote
40	7	2.8	162	2	T24937	hypothetical prote
41	7	2.8	162	2	T31173	hypothetical prote
42	7	2.8	164	2	S76920	hypothetical prote
43	7	2.8	170	2	S44789	D2007.4 protein -
44	7	2.8	174	2	D87638	transcription regu
45	7	2.8	180	1	LGGT	beta-lactoglobulin

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OM protein - protein search, using sw model

Run on: December 21, 2004, 16:29:02 ; Search time 63.038 Seconds
(without alignments)
2272.730 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284
Perfect score: 249
Sequence: 1 MAARRSQRRGRRGEPEGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	249	100.0	249	1	TN12_HUMAN	O43508 homo sapien
2	166	66.7	330	2	Q8IZK7	Q8izk7 homo sapien
3	124	49.8	134	2	Q6IPN8	Q6ipn8 homo sapien
4	124	49.8	134	2	AAH71837	Aah71837 homo sapi
5	32	12.9	249	1	TN12_MOUSE	O54907 mus musculu
6	32	12.9	410	2	Q8BXS2	Q8bxs2 mus musculu
7	27	10.8	249	2	Q6J1A8	Q6j1a8 rattus norv
8	27	10.8	249	2	AAT35582	Aat35582 rattus no
9	12	4.8	438	2	Q7VVB7	Q7vvb7 bordetella
10	12	4.8	470	2	Q7W7F2	Q7w7f2 bordetella
11	10	4.0	61	2	Q6NDU2	Q6ndu2 rhodopseuso
12	10	4.0	61	2	CAE25456	Cae25456 rhodopseu
13	10	4.0	111	1	YFBW_ECOLI	Q47377 escherichia
14	10	4.0	111	2	Q7UC61	Q7uc61 shigella fl
15	10	4.0	111	2	Q8FFL8	Q8ffl8 escherichia
16	10	4.0	111	2	Q8X4J8	Q8x4j8 escherichia

17	9	3.6	142	2	Q98IJ0	Q98ij0 rhizobium 1
18	9	3.6	414	2	Q6TNW7	Q6tnw7 pavlova gyr
19	9	3.6	414	2	AAR30310	Aar30310 pavlova g
20	9	3.6	422	2	Q6TNW5	Q6tnw5 heterosigma
21	9	3.6	422	2	Q6TNW6	Q6tnw6 pavlova lut
22	9	3.6	422	2	Q6TNY6	Q6tny6 cyanidium s
23	9	3.6	422	2	AAR30291	Aar30291 cyanidium
24	9	3.6	422	2	AAR30311	Aar30311 pavlova 1
25	9	3.6	422	2	AAR30312	Aar30312 heterosig
26	9	3.6	733	1	PSAB_ODOSI	P49480 odontella s
27	9	3.6	734	1	PSAB_CYACA	Q9tlq6 cyanidium c
28	9	3.6	749	2	Q7V511	Q7v511 prochloroco
29	9	3.6	766	2	Q8PPZ8	Q8ppz8 xanthomonas
30	9	3.6	1208	2	Q7ULK4	Q7ulk4 rhodopirell
31	8	3.2	58	1	HSP1_CHRPI	Q7lzb2 chrysemys p
32	8	3.2	72	2	Q7Q4R0	Q7q4r0 anopheles g
33	8	3.2	112	2	Q7NN48	Q7nn48 gloeobacter
34	8	3.2	123	2	Q7PM76	Q7pm76 anopheles g
35	8	3.2	143	2	Q9HST7	Q9hst7 halobacteri
36	8	3.2	151	2	Q9SDI1	Q9sdi1 oryza sativ
37	8	3.2	154	2	Q848K4	Q848k4 uncultured
38	8	3.2	179	1	ADHS_GLUOX	O05544 gluconobact
39	8	3.2	190	2	Q8DZK5	Q8dzk5 streptococc
40	8	3.2	190	2	Q8E569	Q8e569 streptococc
41	8	3.2	193	2	Q8L4K2	Q8l4k2 oryza sativ
42	8	3.2	211	2	Q9VV70	Q9vv70 drosophila
43	8	3.2	211	2	Q8SXH4	Q8sxh4 drosophila
44	8	3.2	220	1	Y304_BRUME	Q8yd73 brucella me
45	8	3.2	220	1	Y3J1_BRUSU	Q8fv59 brucella su

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OM protein - protein search, using sw model

Run on: December 21, 2004, 13:32:14 ; Search time 56.7342 Seconds
(without alignments)
1574.423 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284
Perfect score: 1268
Sequence: 1 MAARRSQRRGRRGEPGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1268	100.0	249	2	AAY09369	Aay09369 Human tum
2	1268	100.0	249	3	AAY95338	Aay95338 Human PRO
3	1268	100.0	249	3	AAB07526	Aab07526 Amino aci
4	1268	100.0	249	5	AAU86129	Aau86129 Human PRO
5	1268	100.0	249	6	ABR42315	Abr42315 Human TWE
6	1268	100.0	249	7	ADC35206	Adc35206 Human TNF
7	1268	100.0	249	7	ABW02278	Abw02278 Human TWE
8	1268	100.0	249	7	ADJ37285	Adj37285 Human tum
9	1268	100.0	249	8	ADG68209	Adg68209 Human PRO

10	1268	100.0	284	2	AAW47525	Aaw47525 Homo sapi
11	1265	99.8	249	2	AAW29745	Aaw29745 TNF relat
12	1265	99.8	249	4	AAE00891	Aae00891 Human TRE
13	1135	89.5	249	7	ADC97712	Adc97712 Murine FL
14	1066	84.1	273	4	AAU03499	Aau03499 TWEAK ext
15	1062	83.8	208	2	AAW93590	Aaw93590 Human TNR
16	1020	80.4	225	2	AAW47524	Aaw47524 Mus muscu
17	1020	80.4	225	3	AAB07527	Aab07527 Amino aci
18	968	76.3	211	2	AAW93591	Aaw93591 Mouse TNR
19	792	62.5	189	2	AAW29746	Aaw29746 TNF relat
20	792	62.5	189	4	AAE00892	Aae00892 Human UL4
21	761	60.0	146	4	AAE00895	Aae00895 Human TRE
22	116	9.1	325	4	ABB67553	Abb67553 Drosophil
23	116	9.1	409	5	AAU77718	Aau77718 Drosophil
24	108.5	8.6	211	3	AAY58216	Aay58216 Canine ma
25	108.5	8.6	260	3	AAY58215	Aay58215 Canine CD
26	105.5	8.3	406	5	AAU77717	Aau77717 Drosophil
27	104	8.2	409	5	AAU77716	Aau77716 Drosophil
28	102.5	8.1	603	7	ABO76518	Abo76518 Pseudomon
29	101.5	8.0	681	7	ABO72807	Abo72807 Pseudomon
30	100	7.9	220	4	AAB62340	Aab62340 Gp120 V3
31	96	7.6	234	4	AAB62339	Aab62339 Gp120 V3
32	95.5	7.5	254	2	AAR64190	Aar64190 Human 4-1
33	95.5	7.5	254	2	AAW26657	Aaw26657 Human 4-1
34	95.5	7.5	254	5	ABB75953	Abb75953 Human cyt
35	95.5	7.5	254	6	ABR42312	Abr42312 Human 4-1
36	95.5	7.5	254	7	ADC35200	Adc35200 Human TNF
37	95.5	7.5	254	7	ADD18780	Add18780 Human dis
38	95.5	7.5	254	7	ABW02275	Abw02275 Human 4-1
39	95.5	7.5	254	7	ADJ68703	Adj68703 Human hea
40	95.5	7.5	254	8	ADG63846	Adg63846 Human CD1
41	95.5	7.5	254	8	ADL24281	Adl24281 Human 4-1
42	94.5	7.5	240	5	AAE13680	Aae13680 Human HVE
43	94	7.4	448	6	ABU41896	Abu41896 Protein e
44	93.5	7.4	281	8	ADO24768	Ado24768 Cat TRAIL
45	93.5	7.4	876	4	ABG00217	Abg00217 Novel hum

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OM protein - protein search, using sw model

Run on: December 21, 2004, 16:11:02 ; Search time 15.7595 Seconds
(without alignments)
1520.225 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284
Perfect score: 1268
Sequence: 1 MAARRSQRRGRRGEPGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	95.5	7.5	254	2	I38427
2	95	7.5	375	2	A75264
3	93.5	7.4	776	2	T36946
4	93.5	7.4	1657	2	T15838
5	93	7.3	378	2	H87333
6	91.5	7.2	212	2	A70611
7	90	7.1	441	2	S41710
8	90	7.1	660	2	T03038
9	89	7.0	664	2	D83231
10	87	6.9	197	1	JH0309
11	87	6.9	204	1	S24641
12	87	6.9	310	2	D70745
13	87	6.9	445	2	T30604
14	86.5	6.8	755	2	B75346

15	86.5	6.8	762	2	E98121	hypothetical prote
16	86.5	6.8	764	1	S14113	1-phosphatidylinos
17	86.5	6.8	810	2	D95256	ATP-dependent Clp
18	86	6.8	139	2	B69953	hypothetical prote
19	86	6.8	878	2	T17245	hypothetical prote
20	86	6.8	1323	2	S27224	N-methyl-D-asparta
21	85	6.7	431	2	T01557	hypothetical prote
22	84.5	6.7	933	1	B48349	glycoprotein B pre
23	84.5	6.7	9376	2	T14593	syringomycin synth
24	84	6.6	260	2	T45750	ribosomal protein
25	84	6.6	274	2	S71527	outer surface prot
26	84	6.6	566	2	T35203	probable two-compo
27	83.5	6.6	885	1	VGBESA	glycoprotein B pre
28	83	6.5	206	2	T34961	probable membrane
29	83	6.5	228	2	B83583	dethiobiotin synth
30	83	6.5	439	2	B70629	hypothetical prote
31	83	6.5	520	2	E87621	hypothetical prote
32	83	6.5	531	2	C83153	conserved hypothet
33	83	6.5	565	2	G98331	probable oligopept
34	83	6.5	936	2	S43738	transcription acti
35	82.5	6.5	210	2	D87394	hypothetical prote
36	82	6.5	258	2	C84559	60S ribosomal prot
37	82	6.5	352	2	T08209	matrix protein - H
38	82	6.5	422	2	S32357	glial growth facto
39	82	6.5	467	2	G82697	hypothetical prote
40	82	6.5	563	2	AE3059	hypothetical prote
41	82	6.5	563	2	C98227	hypothetical prote
42	81.5	6.4	260	2	S22641	ribosomal protein
43	81	6.4	244	2	A46066	lymphotoxin beta -
44	81	6.4	273	2	S51108	outer surface prot
45	81	6.4	681	2	H83044	2,4-dienoyl-CoA re

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OM protein - protein search, using sw model

Run on: December 21, 2004, 15:00:12 ; Search time 61.9873 Seconds
(without alignments)
2311.251 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284

Perfect score: 1268

Sequence: 1 MAARRSQRRRGRGEPEGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1268	100.0	249	1	TN12_HUMAN	O43508 homo sapien
2	1135	89.5	249	1	TN12_MOUSE	O54907 mus musculu
3	1105	87.1	249	2	Q6J1A8	Q6j1a8 rattus norv
4	1105	87.1	249	2	AAT35582	Aat35582 rattus no
5	937.5	73.9	410	2	Q8BXS2	Q8bxs2 mus musculu
6	844	66.6	330	2	Q8IZK7	Q8izk7 homo sapien
7	621	49.0	134	2	Q6IPN8	Q6ipn8 homo sapien
8	621	49.0	134	2	AAH71837	Aah71837 homo sapi
9	116	9.1	261	2	Q8MRW2	Q8mrw2 drosophila
10	116	9.1	409	2	Q8MY88	Q8my88 drosophila
11	116	9.1	409	2	AAS64883	Aas64883 drosophil
12	116	9.1	415	2	Q9V5G2	Q9v5g2 drosophila
13	116	9.1	415	2	AAF58848	Aaf58848 drosophil
14	113	8.9	409	2	Q8IGD3	Q8igd3 drosophila
15	109.5	8.6	272	1	TNF5_CHICK	Q9i8d8 gallus gall
16	108.5	8.6	260	1	TNF5_CANFA	O97626 canis famil

17	108.5	8.6	260	2	AAP86654	Aap86654 canis fam
18	99	7.8	532	2	Q82HP6	Q82hp6 streptomyce
19	97.5	7.7	694	2	Q82FL1	Q82fl1 streptomyce
20	97	7.6	643	2	Q9KZ17	Q9kz17 streptomyce
21	95.5	7.5	201	1	TNFB_MACEU	Q9xt48 macropus eu
22	95.5	7.5	254	1	TNF9_HUMAN	P41273 homo sapien
23	95	7.5	375	2	Q9RRH5	Q9rrh5 deinococcus
24	95	7.5	390	2	Q8KW28	Q8kw28 ruegeria sp
25	95	7.5	776	2	Q6Y659	Q6y659 burkholderi
26	95	7.5	776	2	AAO19443	Aao19443 burkholde
27	94	7.4	448	2	Q886A1	Q886a1 pseudomonas
28	94	7.4	937	2	Q93JD1	Q93jd1 streptomyce
29	93.5	7.4	776	2	Q9RJ01	Q9rj01 streptomyce
30	93	7.3	378	2	Q9AAB9	Q9aab9 caulobacter
31	93	7.3	449	2	Q7UMG0	Q7umg0 rhodopirell
32	92.5	7.3	720	2	Q6FEP2	Q6fep2 acinetobact
33	92	7.3	304	2	Q7T1F2	Q7t1f2 gallus gall
34	92	7.3	977	2	Q8TET1	Q8tet1 homo sapien
35	91.5	7.2	212	2	O86312	O86312 mycobacteri
36	91.5	7.2	212	2	Q7U0D1	Q7u0d1 mycobacteri
37	91.5	7.2	213	2	Q82AD2	Q82ad2 streptomyce
38	91.5	7.2	240	1	TN14_HUMAN	O43557 homo sapien
39	91.5	7.2	394	2	Q8LQH5	Q8lqh5 oryza sativ
40	91.5	7.2	718	2	Q89W68	Q89w68 bradyrhizob
41	90.5	7.1	251	2	Q7WA78	Q7wa78 bordetella
42	90.5	7.1	439	2	Q72LQ4	Q72lq4 thermus the
43	90.5	7.1	439	2	AAS80352	Aas80352 thermus t
44	90.5	7.1	1100	2	Q937L3	Q937l3 deinococcus
45	90	7.1	369	2	Q747J1	Q747j1 geobacter s

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 18:47:38 ; Search time 4490.4 Seconds
(without alignments)
2622.288 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284

Perfect score: 249

Sequence: 1 MAARRSQRRRGRRGEPGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9045947

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-
Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162224_10205/app_query.fasta_1.7
82
-DB=GenEmbl -QFMT=fastap -SUFFIX=olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198@CGN_1_1_4236@runat_20122004_162224_10205 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

```

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	249	100.0	1306	9	AF030099	AF030099 Homo sapi
2	249	100.0	1353	6	AX201324	AX201324 Sequence
3	249	100.0	1353	9	AY358870	AY358870 Homo sapi
4	249	100.0	1368	9	AF055872	AF055872 Homo sapi
5	249	100.0	1373	6	BD062758	BD062758 A tumor n
6	249	100.0	1421	6	BD090952	BD090952 Apo-3 lig
7	241	96.8	1236	6	AR140407	AR140407 Sequence
8	241	96.8	1236	6	BD057124	BD057124 Member of
9	207	83.1	898	6	AX180714	AX180714 Sequence
10	166	66.7	1816	9	AY081051	AY081051 Homo sapi
11	125	50.2	1615	9	BC071837	BC071837 Homo sapi
12	125	50.2	1642	9	BC019047	BC019047 Homo sapi
c 13	84	33.7	60268	9	AC016876	AC016876 Homo sapi
c 14	84	33.7	218485	2	AC127470	AC127470 Pan trogl
c 15	68	27.3	751	11	BV166827	BV166827 TNFSF12_2
c 16	32	12.9	1168	6	BD062757	BD062757 A tumor n
c 17	32	12.9	1239	10	AF030100	AF030100 Mus muscu
c 18	32	12.9	1576	10	BC079107	BC079107 Rattus no
c 19	32	12.9	130254	2	AC136195	AC136195 Rattus no
c 20	32	12.9	149736	2	AC126239	AC126239 Felis cat
c 21	32	12.9	165316	2	AC119115	AC119115 Rattus no
c 22	32	12.9	180222	2	AC130192	AC130192 Sus scrof
c 23	32	12.9	203083	2	AC069459	AC069459 Mus muscu
c 24	32	12.9	223877	2	AC098923	AC098923 Rattus no
c 25	32	12.9	225077	2	AC136563	AC136563 Rattus no
c 26	32	12.9	234182	10	AL603707	AL603707 Mouse DNA
c 27	32	12.9	234801	2	AC118309	AC118309 Rattus no
c 28	31	12.4	176258	2	AC126925	AC126925 Canis fam
c 29	27	10.8	750	10	AY607588	AY607588 Rattus no
c 30	26	10.4	201	11	BV202888	BV202888 sqnm21025
c 31	19	7.6	148555	2	AC126921	AC126921 Bos tauru
c 32	17	6.8	212093	2	AC126237	AC126237 Canis fam
c 33	16	6.4	50	6	AX201395	AX201395 Sequence
c 34	16	6.4	50	6	BD090954	BD090954 Apo-3 lig
c 35	12	4.8	346274	1	BX640443	BX640443 Bordetell
c 36	12	4.8	348014	1	BX640430	BX640430 Bordetell
c 37	12	4.8	349672	1	BX640419	BX640419 Bordetell
c 38	11	4.4	1272	1	AB075553	AB075553 Gordonia
c 39	11	4.4	1272	1	AB075555	AB075555 Gordonia
c 40	10	4.0	219	5	GGC062	X59899 G.gallus CO
c 41	10	4.0	365	11	BV030078	BV030078 S212P6009
c 42	10	4.0	531	8	AF123564	AF123564 Helianthu
c 43	10	4.0	2085	8	AF123558	AF123558 Helianthu

44 10 4.0 9966 1 AE015249
45 10 4.0 13606 1 AE005458.

AE015249 Shigella
AE005458 Escherich

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 17:01:58 ; Search time 500.627 Seconds
(without alignments)
2610.940 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284

Perfect score: 249

Sequence: 1 MAARRSQRRRGRRGEPGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8266295

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-

Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162224_10195/app_query.fasta_1.7
82
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198_@CGN_1_1_586_@runat_20122004_162224_10195 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	249	100.0	1306	8	ACC57901	Acc57901 Human TWE
2	249	100.0	1306	10	ADC35205	Adc35205 Human cDN
3	249	100.0	1306	10	AAD63914	Aad63914 Human TWE
4	249	100.0	1306	10	ACC57587	Acc57587 Polynucle
5	249	100.0	1353	3	AAA49717	Aaa49717 Human PRO
6	249	100.0	1353	6	ABK40255	Abk40255 cDNA enco
7	249	100.0	1353	10	ADJ37284	Adj37284 Human tum
8	249	100.0	1353	12	ADG68208	Adg68208 Human PRO
9	249	100.0	1364	6	ABK34881	Abk34881 Human cDN
10	249	100.0	1373	2	AAV18600	Aav18600 Homo sapi
11	249	100.0	1421	2	AAX56000	Aax56000 Human tum
12	241	96.8	1236	2	AAV47613	Aav47613 TNF relat
13	241	96.8	1236	4	AAD04350	Aad04350 Human TRE
14	207	83.1	898	4	AAS03964	Aas03964 Expressio
15	107	43.0	1030	2	AAX23424	Aax23424 Human TNR
16	46	18.5	701	2	AAX23425	Aax23425 Mouse TNR
17	32	12.9	1168	2	AAV18599	Aav18599 Mus muscu
18	32	12.9	1239	10	ADC97713	Adc97713 Murine FL
19	19	7.6	408	8	ABX37032	Abx37032 Bovine ES
20	16	6.4	50	2	AAX56002	Aax56002 Human tum
21	16	6.4	50	3	AAA49732	Aaa49732 Human PRO
22	16	6.4	50	6	ABK40292	Abk40292 Oligonucl
23	16	6.4	50	10	ADJ37355	Adj37355 Tumour th
24	16	6.4	50	12	ADG68279	Adg68279 Human PRO
25	10	4.0	669	8	ACA19172	Aca19172 Prokaryot
c 26	9	3.6	285	4	AAK76903	Aak76903 Human imm
c 27	9	3.6	351	6	ABL91276	Abl91276 Chlamydia
28	9	3.6	402	6	ABL79259	Abl79259 Human ova
29	9	3.6	417	11	ABD05774	Abd05774 Pseudomon
c 30	9	3.6	430	8	ABZ53879	Abz53879 Aspergill
31	9	3.6	434	6	ABZ08449	Abz08449 Human leu
c 32	9	3.6	501	10	ADE60390	Ade60390 Rat gene
c 33	9	3.6	501	10	ADD45854	Add45854 Rat gene
c 34	9	3.6	559	9	ACH15200	Ach15200 Human adu
c 35	9	3.6	632	4	AAH07223	Aah07223 Human cDN
36	9	3.6	662	6	ABQ44648	Abq44648 Oligonucl
c 37	9	3.6	662	6	ABQ44649	Abq44649 Oligonucl
c 38	9	3.6	707	3	AAF12754	Aaf12754 Aspergill
c 39	9	3.6	720	11	ABD05675	Abd05675 Pseudomon
c 40	9	3.6	765	11	ADJ12066	Adj12066 Maize cDN
c 41	9	3.6	935	12	ADH45496	Adh45496 Human mol
42	9	3.6	973	12	ADI42516	Adi42516 Plant tra
c 43	9	3.6	1080	5	AAF99987	Aaf99987 Corynebac
c 44	9	3.6	1080	5	AAH66706	Aah66706 C glutami
c 45	9	3.6	1083	4	AAF25333	Aaf25333 Coding re

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 21:10:13 ; Search time 3327.35 Seconds
(without alignments)
2726.939 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284

Perfect score: 249

Sequence: 1 MAARRSQRRRGRGEPEGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 1

Total number of hits satisfying chosen parameters: 65644297

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-
Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162224_10214/app_query.fasta_1.7
82
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198@CGN_1_1_4385@runat_20122004_162224_10214 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	188	75.5	777	4	BI819200	BI819200 603034614
2	183	73.5	666	6	CF126539	CF126539 UI-HF-ET0
3	181	72.7	545	6	CB141389	CB141389 K-EST0194
4	172	69.1	567	6	CA396679	CA396679 cs80h07.y
5	169	67.9	728	4	BI870393	BI870393 603395641
6	169	67.9	731	4	BI871711	BI871711 603395825
7	166	66.7	697	6	CF126932	CF126932 UI-HF-ET0
8	152	61.0	834	4	BI766766	BI766766 603056866
9	148	59.4	963	5	BQ671259	BQ671259 AGENCOURT
10	147	59.0	1071	4	BM921213	BM921213 AGENCOURT
11	145	58.2	940	5	BQ884231	BQ884231 AGENCOURT
12	126	50.6	948	5	BQ707185	BQ707185 AGENCOURT
13	119	47.8	824	6	CB998034	CB998034 AGENCOURT
14	119	47.8	828	4	BI596681	BI596681 603243254
15	116	46.6	951	5	BQ674188	BQ674188 AGENCOURT
16	96	38.6	298	4	BM688946	BM688946 UI-E-CQ1-
17	84	33.7	776	5	BX090012	BX090012 BX090012
18	72	28.9	698	4	BI906850	BI906850 603064633
19	70	28.1	894	4	BI908274	BI908274 603068526
20	63	25.3	456	4	BI966255	BI966255 ie72g04.y
21	60	24.1	785	4	BI762908	BI762908 603047966
22	59	23.7	587	4	BG686319	BG686319 602638232
23	54	21.7	345	7	R55379	R55379 yj77a08.r1
24	53	21.3	1064	7	CF994566	CF994566 AGENCOURT
25	53	21.3	1319	7	CF594233	CF594233 AGENCOURT
26	47	18.9	910	4	BG110063	BG110063 602279667
27	40	16.1	465	1	AI091441	AI091441 cw62g05.x
28	38	15.3	538	2	BF821434	BF821434 MR1-RT003
29	36	14.5	531	4	BI824443	BI824443 603038693
30	33	13.3	918	2	BF577781	BF577781 602092080
C	31	32	12.9	315	2	BF466521
	32	32	12.9	349	6	BY766420
	33	32	12.9	360	2	BE654876
	34	32	12.9	445	1	AA870722
	35	32	12.9	482	9	CG653257
C	36	32	12.9	487	2	AW320117
	37	32	12.9	493	2	BE307031
	38	32	12.9	494	9	CG596702
	39	32	12.9	531	9	CG590009
	40	32	12.9	533	2	BE628951
	41	32	12.9	543	9	CG565104
	42	32	12.9	554	9	CG629394
	43	32	12.9	558	4	BM484863
	44	32	12.9	561	2	AW763237
45	32	12.9	620	7	CK625052	CK625052 mi28e10.y

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 16:43:23 ; Search time 4489.88 Seconds
(without alignments)
2622.595 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284

Perfect score: 1268

Sequence: 1 MAARRSQRRGRRGEPGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-

Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162203_9562/app_query.fasta_1.78
2
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198_@CGN_1_1_4236_@runat_20122004_162203_9562 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

```

11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description	
No.	Score	Match	Length	DB	ID		
1	1268	100.0	1306	9	AF030099	AF030099 Homo sapi	
2	1268	100.0	1353	6	AX201324	AX201324 Sequence	
3	1268	100.0	1353	9	AY358870	AY358870 Homo sapi	
4	1268	100.0	1368	9	AF055872	AF055872 Homo sapi	
5	1268	100.0	1373	6	BD062758	BD062758 A tumor n	
6	1268	100.0	1421	6	BD090952	BD090952 Apo-3 lig	
7	1265	99.8	1236	6	AR140407	AR140407 Sequence	
8	1265	99.8	1236	6	BD057124	BD057124 Member of	
9	1193.5	94.1	1615	9	BC071837	BC071837 Homo sapi	
10	1193.5	94.1	1642	9	BC019047	BC019047 Homo sapi	
11	1135	89.5	1239	10	AF030100	AF030100 Mus muscu	
12	1113	87.8	1576	10	BC079107	BC079107 Rattus no	
13	1105	87.1	750	10	AY607588	AY607588 Rattus no	
14	1066	84.1	898	6	AX180714	AX180714 Sequence	
15	1020	80.4	1168	6	BD062757	BD062757 A tumor n	
16	844	66.6	1816	9	AY081051	AY081051 Homo sapi	
c	17	589.5	46.5	60268	9	AC016876	AC016876 Homo sapi
	18	589.5	46.5	218485	2	AC127470	AC127470 Pan trogl
	19	571.5	45.1	130254	2	AC136195	AC136195 Rattus no
c	20	571.5	45.1	165316	2	AC119115	AC119115 Rattus no
	21	571.5	45.1	223877	2	AC098923	AC098923 Rattus no
c	22	571.5	45.1	225077	2	AC136563	AC136563 Rattus no
c	23	571.5	45.1	234801	2	AC118309	AC118309 Rattus no
	24	562	44.3	180222	2	AC130192	AC130192 Sus scrof
	25	556.5	43.9	149736	2	AC126239	AC126239 Felis cat
	26	555.5	43.8	176258	2	AC126925	AC126925 Canis fam
c	27	555.5	43.8	203083	2	AC069459	AC069459 Mus muscu
c	28	555.5	43.8	234182	10	AL603707	AL603707 Mouse DNA
	29	495	39.0	148555	2	AC126921	AC126921 Bos tauru
	30	346	27.3	751	11	BV166827	BV166827 TNFSF12_2
	31	238	18.8	212093	2	AC126237	AC126237 Canis fam
c	32	151	11.9	170189	2	BX957358	BX957358 Danio rer
	33	151	11.9	237644	2	CR318653	CR318653 Danio rer
	34	142	11.2	201	11	BV202888	BV202888 sqnm21025
	35	135.5	10.7	187835	8	AP002482	AP002482 Oryza sat
	36	124	9.8	310550	1	SCO939113	AL939113 Streptomy
c	37	122	9.6	308050	1	SCO939124	AL939124 Streptomy
	38	121	9.5	6397	1	AF002222	AF002222 Pseudomon
	39	121	9.5	10728	1	AE004651	AE004651 Pseudomon
c	40	118.5	9.3	190050	1	AL646059	AL646059 Ralstonia
	41	116	9.1	978	6	CQ601692	CQ601692 Sequence
	42	116	9.1	1221	3	AY119233	AY119233 Drosophil
	43	116	9.1	1248	3	AY115551	AY115551 Drosophil

44 116 9.1 1656 3 AB073865
45 116 9.1 2101 3 AF149799

AB073865 Drosophil
AF149799 Drosophil

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 16:40:38 ; Search time 501.152 Seconds
(without alignments)
2608.203 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284

Perfect score: 1268

Sequence: 1 MAARRSQRRRGRGEPEGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-
Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162203_9545/app_query.fasta_1.78
2
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198@CGN_1_1_586@runat_20122004_162203_9545 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	
	1	1268	100.0	1306	8	ACC57901	Acc57901 Human TWE
	2	1268	100.0	1306	10	ADC35205	Adc35205 Human cDN
	3	1268	100.0	1306	10	AAD63914	Aad63914 Human TWE
	4	1268	100.0	1306	10	ACC57587	Acc57587 Polynucle
	5	1268	100.0	1353	3	AAA49717	Aaa49717 Human PRO
	6	1268	100.0	1353	6	ABK40255	Abk40255 cDNA enco
	7	1268	100.0	1353	10	ADJ37284	Adj37284 Human tum
	8	1268	100.0	1353	12	ADG68208	Adg68208 Human PRO
	9	1268	100.0	1364	6	ABK34881	Abk34881 Human cDN
	10	1268	100.0	1373	2	AAV18600	Aav18600 Homo sapi
	11	1268	100.0	1421	2	AAX56000	Aax56000 Human tum
	12	1265	99.8	1236	2	AAV47613	Aav47613 TNF relat
	13	1265	99.8	1236	4	AAD04350	Aad04350 Human TRE
	14	1135	89.5	1239	10	ADC97713	Adc97713 Murine FL
	15	1066	84.1	898	4	AAS03964	Aas03964 Expressio
	16	1062	83.8	1030	2	AAX23424	Aax23424 Human TNR
	17	1020	80.4	1168	2	AAV18599	Aav18599 Mus muscu
	18	968	76.3	701	2	AAX23425	Aax23425 Mouse TNR
	19	466	36.8	408	8	ABX37032	Abx37032 Bovine ES
	20	129.5	10.2	264	8	ABX52254	Abx52254 Bovine ES
	21	116	9.1	978	4	ABL21473	Ab121473 Drosophil
	22	116	9.1	2148	6	ABK11680	Abk11680 DNA encod
	23	111	8.8	1554	11	ABD10189	Abd10189 Pseudomon
	24	111	8.8	1812	11	ABD10089	Abd10089 Pseudomon
c	25	111	8.8	2667	11	ABD10650	Abd10650 Pseudomon
	26	111	8.8	2856	2	AAV24140	Aav24140 Homo sapi
	27	109.5	8.6	1317	12	ADJ44494	Adj44494 Plant cDN
	28	109.5	8.6	1660	3	AAA49205	Aaa49205 Corn puta
	29	109.5	8.6	2166	6	ABK11678	Abk11678 DNA encod
c	30	108.5	8.6	633	3	AAZ55539	Aaz55539 Canine ma
	31	108.5	8.6	633	3	AAZ55538	Aaz55538 Canine ma
	32	108.5	8.6	780	3	AAZ55536	Aaz55536 Canine CD
c	33	108.5	8.6	780	3	AAZ55537	Aaz55537 Canine CD
	34	108.5	8.6	1878	3	AAZ55534	Aaz55534 Canine CD
c	35	108.5	8.6	1878	3	AAZ55535	Aaz55535 Canine CD
	36	108	8.5	1344	8	ACA45766	Aca45766 Prokaryot
c	37	108	8.5	3880	6	ABL67211	Ab167211 Thyroid c
c	38	108	8.5	3880	8	ACC50307	Acc50307 Breast ca
c	39	108	8.5	3901	2	AAT42224	Aat42224 Human TAT
c	40	108	8.5	3901	2	AAT79598	Aat79598 TATA-bind
c	41	108	8.5	3902	2	AAQ70738	Aaq70738 TATA-bind
	42	107.5	8.5	1257	11	ABD15611	Abd15611 Pseudomon
	43	107.5	8.5	1266	11	ABD15567	Abd15567 Pseudomon
c	44	107.5	8.5	1566	11	ABD15448	Abd15448 Pseudomon
	45	107	8.4	741	11	ABD06733	Abd06733 Pseudomon

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2004, 16:42:43 ; Search time 3327.88 Seconds
(without alignments)
2726.509 Million cell updates/sec

Title: US-09-245-198A-4_COPY_36_284

Perfect score: 1268

Sequence: 1 MAARRSQRRRGRRGEPGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

- Q=/cgn2_1/USPTO_spool/US09245198/runat_20122004_162203_9569/app_query.fasta_1.78

2

-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09245198@CGN_1_1_4385@runat_20122004_162203_9569 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1087.5	85.8	731	4	BI871711	BI871711 603395825
2	1060.5	83.6	728	4	BI870393	BI870393 603395641
3	1032.5	81.4	697	6	CF126932	CF126932 UI-HF-ETO
4	979	77.2	777	4	BI819200	BI819200 603034614
5	976	77.0	790	7	CO559990	CO559990 AGENCOURT
6	969	76.4	666	6	CF126539	CF126539 UI-HF-ETO
7	962	75.9	834	4	BI766766	BI766766 603056866
8	941	74.2	545	6	CB141389	CB141389 K-EST0194
9	937.5	73.9	2237	3	AK044387	AK044387 Mus muscu
10	935.5	73.8	760	7	CO572381	CO572381 AGENCOURT
11	934	73.7	828	4	BI596681	BI596681 603243254
12	913	72.0	918	2	BF577781	BF577781 602092080
13	909.5	71.7	948	5	BQ707185	BQ707185 AGENCOURT
14	904	71.3	940	5	BQ884231	BQ884231 AGENCOURT
15	900	71.0	805	7	CO393621	CO393621 AGENCOURT
16	899.5	70.9	620	7	CK625052	CK625052 mi28e10.y
17	879	69.3	567	6	CA396679	CA396679 cs80h07.y
18	842	66.4	748	7	CN270781	CN270781 170005999
19	825	65.1	561	2	AW763237	AW763237 ur70d09.y
20	813.5	64.2	774	7	CO574209	CO574209 AGENCOURT
21	809	63.8	963	5	BQ671259	BQ671259 AGENCOURT
22	765	60.3	1071	4	BM921213	BM921213 AGENCOURT
23	753	59.4	951	5	BQ674188	BQ674188 AGENCOURT
24	738	58.2	543	9	CG565104	CG565104 OST189654
25	723	57.0	482	9	CG653257	CG653257 OST418407
26	716.5	56.5	785	4	BI762908	BI762908 603047966
27	707	55.8	665	6	BY742288	BY742288 BY742288
28	707	55.8	1033	3	AK020909	AK020909 Mus muscu
29	702.5	55.4	824	6	CB998034	CB998034 AGENCOURT
30	681	53.7	498	9	CG554711	CG554711 OST168603
31	652	51.4	584	2	AW917574	AW917574 EST348878
32	649.5	51.2	704	7	CK357507	CK357507 AGENCOURT
33	647	51.0	939	6	CB849011	CB849011 MRA-0673
34	635.5	50.1	894	4	BI908274	BI908274 603068526
35	624.5	49.3	621	9	CG584545	CG584545 OST230701
36	623.5	49.2	1064	7	CF994566	CF994566 AGENCOURT
37	618.5	48.8	474	9	CG609156	CG609156 OST290052
38	607	47.9	418	9	CG611020	CG611020 OST295426
39	604	47.6	445	1	AA870722	AA870722 vq25g07.r
40	601	47.4	483	9	CG646715	CG646715 OST393421
41	600	47.3	587	4	BG686319	BG686319 602638232
42	598.5	47.2	471	1	AA221610	AA221610 my18d09.r
43	598	47.2	892	6	CB204861	CB204861 AGENCOURT
44	597.5	47.1	531	9	CG590009	CG590009 OST242925
45	596	47.0	494	9	CG596702	CG596702 OST259234